

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:37:52 ; Search time 38 Seconds
(without alignments)
3513.646 Million cell updates/sec

Title: US-09-637-302C-2

Perfect score: 3413

Sequence: 1 MEHIGAKMTISNGFGKDA.....AHTEDINACTLTTSPLRVF 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_cheap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3331	97.6	648	11 Q99N57	Q99N57 mus musculus
2	2786.5	81.6	635	13 Q98TC3	Q98TC3 seriola qui
3	2542	74.5	495	11 Q99N58	Q99N58 mus musculus
4	2185	64.0	421	4 Q15278	Q15278 homo sapien
5	2106.5	61.7	420	13 Q90893	Q90893 gallus gall
6	1895.5	55.5	506	15 Q85632	Q85632 avian retro
7	1890.5	55.4	604	11 Q99J44	Q99J44 mus musculus
8	1886	55.3	609	4 Q96115	Q96115 homo sapien
9	1873.5	54.9	375	15 Q67624	Q67624 ic4 retrovi
10	1685	49.4	651	4 Q9Y6T3	Q9Y6T3 homo sapien
11	1675	49.1	359	15 Q85453	Q85453 murine sarc
12	1577	46.2	308	11 Q9CU36	Q9CU36 mus musculus
13	1573	46.1	301	6 Q19055	Q19055 papio hamad
14	1398.5	41.0	307	13 Q90458	Q90458 brachydanio
15	1391.5	40.8	285	13 Q9DEB2	Q9DEB2 seriola qui
16	1384	40.6	739	5 Q9W4Z3	Q9W4Z3 drosophila

17	1384	40.6	782	5 Q9NEH9	Q9NEH9 drosophila
18	1121.5	32.9	813	5 Q9N4E3	Q9N4E3 caenorhabdi
19	982.5	28.8	246	13 Q98TC4	Q98TC4 seriola qui
20	853	25.0	177	13 Q90W60	Q90W60 seriola qui
21	801	23.5	180	11 Q99MC6	Q99MC6 rattus norv
22	774	22.7	183	13 Q98TC5	Q98TC5 seriola qui
23	748	21.9	146	11 Q99N73	Q99N73 mus musculu
24	697	20.4	580	5 Q9GT28	Q9GT28 brugia mala
25	604	17.7	283	11 Q9CTT5	Q9CTT5 mus musculu
26	575	16.8	966	5 Q24170	Q24170 drosophila
27	575	16.8	966	5 Q24171	Q24171 drosophila
28	569.5	16.7	1003	5 Q24734	Q24734 drosophila
29	554	16.2	873	11 Q61097	Q61097 mus musculu
30	547.5	16.0	373	11 Q9JJU6	Q9JJU6 mus musculu
31	536	15.7	143	13 Q98TD5	Q98TD5 seriola qui
32	525.5	15.4	635	4 Q13476	Q13476 homo sapien
33	502	14.7	97	11 Q8V185	Q8V185 mus musculu
34	493.5	14.5	553	10 Q81808	Q81808 arabidopsis
35	491.5	14.4	546	10 Q22558	Q22558 arabidopsis
36	488.5	14.3	186	11 Q9DBU7	Q9DBU7 mus musculu
37	482	14.1	570	10 Q8RWL6	Q8RWL6 arabidopsis
38	466.5	13.7	1030	10 Q9C9U5	Q9C9U5 arabidopsis
39	465	13.6	847	10 Q93XL9	Q93XL9 rosa hybrid
40	459	13.4	771	5 Q19380	Q19380 caenorhabdi
41	445.5	13.1	806	10 Q9ZSD8	Q9ZSD8 lycopersico
42	445	13.0	829	10 Q9ZSD9	Q9ZSD9 lycopersico
43	440	12.9	829	10 Q24027	Q24027 lycopersico
44	433.5	12.7	483	10 Q8RY96	Q8RY96 arabidopsis
45	429	12.6	903	10 Q9FPR5	Q9FPR5 oryza sativ

ALIGNMENTS

RESULT 1

Q99N57 PRELIMINARY; PRT; 648 AA.
AC Q99N57; Q91WH1;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Protein kinase raf 1 (Similar to murine leukemia viral (V-raf-1)
DE oncogene homolog 1) (3611-MSV).
GN RAF1 OR CRAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Doi M., Abe S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Gray T.A., Azama K., Whitmore K.L., Min A., Abe S., Nicholls R.D.;
RT "A conserved gene antisense to the proto-oncogene c-RAF encodes a
RT multi-zinc-finger protein, MAKORIN2".
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057663; BAB39743.2; -;
DR EMBL; BC015273; AAH15273.1; -;
DR HSSP; P11345; 1RRB.
DR MGD; MGI:97847; Raf1.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR002290; Ser_thr_pkinase.

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DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00130; DAG_PE_bind; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF02196; RBD; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR ProDom: PD000001; Euk_pkinase; 2.
DR SMART: SM00109; C1; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; ATP-binding; Transferase.
SQ SEQUENCE 648 AA; 72917 MW; B70104AEF51C4A45 CRC64;

Query Match      97.6%; Score 3331; DB 11; Length 648;
Best Local Similarity 97.7%; Pred. No. 5.4e-263;
Matches 633; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEHIOGAKWTISNGFGKDAVFDGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIOGAKWTISNGFGLADAVFDGSSCISPTIVQFGYQRRASDDGKLTDSKTSNTIRV 60

QY 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEHKGKARLDWNTDAAS 120

QY 121 LIGELQVDFLDHVPPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSTKV 180
DB 121 LIGELQVDFLDHVPPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSTKV 180

QY 181 PTMCDVNSNIRQLLFPNNTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSPTPHFTF 240
DB 181 PTMCDVNSNIRQLLFPNNTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSPTPHFTF 240

QY 241 NTSSPSSEGSLSQSORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNNL 300
DB 241 NTSSPSSEGSLSQSORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNNL 300

QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKGKWHGDVAVKILKVVDPDTPQFQAFNEVAVLRKTRHVNILFMGYMTKDNLAIV 420
DB 361 GTVYKGKWHGDVAVKILKVVDPDTPQFQAFNEVAVLRKTRHVNILFMGYMTKDNLAIV 420

QY 421 TQWCEGSSLYKHLHVQETKFOFQFOLIDIAQTQAGMDYLHAKNIIHRDMKSNNTFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFOFQFOLIDIAQTQAGMDYLHAKNIIHRDMKSNNTFLHEGL 480

QY 481 TVKIGDFGLAVYKSRWSSQVQOPTGSLVLMWPEVIRMODNPNFQSDVYSIGVLYE 540
DB 481 TVKIGDFGLAVYKSRWSSQVQOPTGSLVLMWPEVIRMODNPNFQSDVYSIGVLYE 540

QY 541 LMTGELPYSHINNRDQIIFVMYGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRDQIIFVMYGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 2
Q98TC3
ID Q98TC3 PRELIMINARY; PRT; 635 AA.
AC Q98TC3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protein kinase raf 1.
GN CRAF.
OS Seriola quinqueradiata (Five-ray yellowtail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Carangidae; Seriola.
OX NCBI_TaxID=8161;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Doi M., Abe S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Gray T.A., Azama K., Whitmore K.L., Min A., Abe S., Nicholls R.D.;
RT "A conserved gene antisense to the proto-oncogene c-Raf encodes a
RT multi-zinc-finger protein, MAKORIN2."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR HSP: P04049; 1PAR.
DR InterPro: IPR002219; DAG_PE_bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003116; RBD.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00130; DAG_PE_bind; 1.
DR Pfam: PF00089; pkinase; 1.
DR Pfam: PF02196; RBD; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PROSITE: PS00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; C1; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 635 AA; 71690 MW; A92D0CB8D855DF5B CRC64;

Query Match      81.6%; Score 2786.5; DB 13; Length 635;
Best Local Similarity 82.1%; Pred. No. 1.4e-218;
Matches 532; Conservative 45; Mismatches 58; Indels 13; Gaps 7;

QY 1 MEHIOGAKWTISNGFGKDAVFDGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIOGAKWTISNGFGKDSAFEG-PCLSPYVQFGPCQRRSSDDSKMPD-SKTSSTIRV 58

QY 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEHKGKARLDWNTDAAS 120

QY 121 LIGELQVDFLDHVPPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSTKV 180
DB 121 LIGELQVDFLDHVPPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSTKV 180

QY 181 PTMCDVNSNIRQLLFPNNTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSPTPHFTF 240
DB 181 PTMCDVNSNIRQLLCP--TPGESGAPSLPPLTSRRMRESLTRFP--SSAHRYSPTPHAFNY 235

QY 241 NTSSPSSEGSLSQSORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNNL 300
DB 241 NTSSPSSEGSLSQSORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNNL 300

QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKGKWHGDVAVKILKVVDPDTPQFQAFNEVAVLRKTRHVNILFMGYMTKDNLAIV 420
DB 361 GTVYKGKWHGDVAVKILKVVDPDTPQFQAFNEVAVLRKTRHVNILFMGYMTKDNLAIV 420

QY 421 TQWCEGSSLYKHLHVQETKFOFQFOLIDIAQTQAGMDYLHAKNIIHRDMKSNNTFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFOFQFOLIDIAQTQAGMDYLHAKNIIHRDMKSNNTFLHEGL 480

QY 481 TVKIGDFGLAVYKSRWSSQVQOPTGSLVLMWPEVIRMODNPNFQSDVYSIGVLYE 540
DB 481 TVKIGDFGLAVYKSRWSSQVQOPTGSLVLMWPEVIRMODNPNFQSDVYSIGVLYE 540

QY 541 LMTGELPYSHINNRDQIIFVMYGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRDQIIFVMYGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
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QY 361 GTVYKGMHGDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILFMGYMTKONLAI 420
DB 349 GTVYKGMHGDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILFMGYMTKONLAI 408
QY 421 TQCEGSSLYKHLHVQETKFOFQOLIDIAQOTAGMDYLHAKNIHROMKSNFIHLEGL 480
DB 409 TQCEGSSLYKHLHVQETKFOFQOLIDIAQOTAGMDYLHAKNIHROMKSNFIHLEGL 468
QY 481 TVKIGDFGLATKVRSGSGSQVQPTGSLVMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
DB 469 TVKIGDFGLATKVRSGSGSQVQPTGSLVMAPEVIRMQDNNPFSQSDVSYGIVLYE 528
QY 541 LMTGELPYSHNNRQDIIIFWVGSGYASPDLSKLYKNCPRKMLVADCVKRYKEERPLFP 600
DB 529 LMTGELPYSHNNRQDIIIFWVGSGYASPDLSKLYKNCPRKMLVADCVKRYKEERPLFP 588
QY 601 QILSSITELQHSPLKPNRSASPSLHRAHTEDINACTLTSPRLPVF 648
DB 589 QILSSITELQHSPLKPNRSASPSLHRAHTEDINACTLTSPRLPVF 635

RESULT 3

Q99N58 PRELIMINARY; PRT; 495 AA.
AC Q99N58
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE Protein kinase raf 1 (Fragment).
GN RAF1 OR CRAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Doi M., Abe S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RT "A conserved gene antisense to the proto-oncogene c-Raf encodes a multi-zinc-finger protein, MAKORIN2.";
CC Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB057655; BAB39748.1; -
DR HSSP; P11345; 1RRB.
DR MGD; MGI:97847; Raf1.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00130; DAG_Pe-bind; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PF02196; RBD; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
FT NON_TER 1
FT NON_TER 495

SQ SEQUENCE 495 AA; 55543 MW; B0AB53C2DAA287AE CRC64;
Query Match 74.5%; Score 2542; DB 11; Length 495;
Best Local Similarity 97.8%; Pred. No. 8.3e-199;
Matches 484; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 11 ISNGFGFDKAVDFDSSCISPTIVQFGYORRASDDGKLTDPSTKSTNTIRVFLPNKQRTVV 70
DB 1 ISNGFGFDKAVDFDSSCISPTIVQFGYORRASDDGKLTDPSTKSTNTIRVFLPNKQRTVV 60
QY 71 NVNRGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAASLIGELQVDF 130
DB 61 NVNRGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAASLIGELQVDF 120
QY 131 LDHVPPLTHNFARKTFELKAFCDICQKFLNGFCQTCGKYKPFHEHCSTKYPTMCDVWSNI 190
DB 121 LDHVPPLTHNFARKTFELKAFCDICQKFLNGFCQTCGKYKPFHEHCSTKYPTMCDVWSNI 180
QY 191 RQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSHPHAFNTSSPSSEGS 250
DB 181 RQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSHPHAFNTSSPSSEGS 240
QY 251 LSQRQSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPALSNNLSPTGWSQPKT 310
DB 241 LSQRQSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPALSNNLSPTGWSQPKT 300
QY 311 PVPQRERAPVSGTQENKIRPRGORDSSYYWEIEASFMVLSLSTRIGSGSGTVYKGMHKG 370
DB 301 PVPQRERAPVSGTQENKIRPRGORDSSYYWEIEASFMVLSLSTRIGSGSGTVYKGMHKG 360
QY 371 DVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILFMGYMTKONLAIYVQWCEGSSLY 430
DB 361 DVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILFMGYMTKONLAIYVQWCEGSSLY 420
QY 431 KHLHVQETKFOFQOLIDIAQOTAGMDYLHAKNIHROMKSNFIHLEGLTVKIGDFGLA 490
DB 421 KHLHVQETKFOFQOLIDIAQOTAGMDYLHAKNIHROMKSNFIHLEGLTVKIGDFGLA 480
QY 491 TVKSRWGSQQVEQP 505
DB 481 TVKSRWGSQQVEQP 495

RESULT 4

Q15278 PRELIMINARY; PRT; 421 AA.
AC Q15278
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE RAF1 protein (Fragment).
GN RAF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85295973; PubMed=2993863;
RA Bonner T.I., Kerby S.B., Sutcliffe P., Gunnell M.A., Mark G., Rapp U.R.;
RT "Structure and biological activity of human homologs of the raf/mil oncogene.";
RL Mol. Cell. Biol. 5:1400-1407(1985).
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; L00212; AAA60247.1; JOINED.
DR EMBL; M11376; AAA60247.1; JOINED.
DR EMBL; L00213; AAA60247.1; JOINED.
DR EMBL; L00206; AAA60247.1; JOINED.
DR EMBL; L00207; AAA60247.1; JOINED.
DR EMBL; L00208; AAA60247.1; JOINED.
DR EMBL; L00209; AAA60247.1; JOINED.
DR EMBL; L00210; AAA60247.1; JOINED.
DR EMBL; L00211; AAA60247.1; JOINED.

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DR HSP; P08631; IAD5.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00221; STYKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 421 AA; 47376 MW; F08DED75D91E8251 CRC64;

Query Match 64.0%; Score 2185; DB 4; Length 421;
Best Local Similarity 99.5%; Pred. No. 8.6e-170;
Matches 419; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 228 SOHRYSTPHAFNTSPSSGSLSORQSTSTPNVHMVSTLPVDSRMIEDAIRSHSES 287
DB 1 SOHRYSTPHAFNTSPSSGSLSORQSTSTPNVHMVSTLPVDSRMIEDAIRSHSES 60
QY 288 ASPSALSSPNNLSPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGQRDSSYYWEIEAS 347
DB 61 ASPSALSSPNNLSPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGQRDSSYYWEIEAS 120
QY 348 EVMLSRIGSGSGFYVYKKGWGDVAVKILKVDPTPEQFAFRNEAVLKRTRHVNILL 407
DB 121 EVMLSRIGSGSGFYVYKKGWGDVAVKILKVDPTPEQFAFRNEAVLKRTRHVNILL 180
QY 408 FMGYMTKDNLAIYVTCWCEGSSLYKHLHVQETKFKFQMFQFLIDIAQTACQMDYLHAKNIHR 467
DB 181 FMGYMTKDNLAIYVTCWCEGSSLYKHLHVQETKFKFQMFQFLIDIAQTACQMDYLHAKNIHR 240
QY 468 DMKSNNIFLHEGLTVKIGDFGLATVKSRSWGSQVQEQPTGSLVWMAPEVIRMQDNNPFSF 527
DB 241 DMKSNNIFLHEGLTVKIGDFGLATVKSRSWGSQVQEQPTGSLVWMAPEVIRMQDNNPFSF 300
QY 528 QSDVSYGIVLYELMTGELPYSHINNRRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVAD 587
DB 301 QSDVSYGIVLYELMTGELPYSHINNRRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVAD 360
QY 588 CVKVKKEERPLFPQILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPV 647
DB 361 CVKVKKEERPLFPQILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPV 420
QY 648 F 648
DB 421 F 421

RESULT 5
Q90893 PRELIMINARY; PRT; 420 AA.
AC Q90893;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE C-mil proto-oncogene, exon 11 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86045899; PubMed=2998016;
RA Jansen H.W., Sister K.;
RT "Nucleotide sequence analysis of the chicken gene c-mil, the
RT progenitor of the retroviral oncogene v-mil.";
RL Virology 143:359-367(1985).
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CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; K03269; AAA48952.1; JOINED.
DR EMBL; K03259; AAA48952.1; JOINED.
DR EMBL; K03260; AAA48952.1; JOINED.
DR EMBL; K03261; AAA48952.1; JOINED.
DR EMBL; K03262; AAA48952.1; JOINED.
DR EMBL; K03263; AAA48952.1; JOINED.
DR EMBL; K03264; AAA48952.1; JOINED.
DR EMBL; K03265; AAA48952.1; JOINED.
DR EMBL; K03266; AAA48952.1; JOINED.
DR EMBL; K03267; AAA48952.1; JOINED.
DR EMBL; K03268; AAA48952.1; JOINED.
DR HSP; P08631; IAD5.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00221; STYKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 420 AA; 47565 MW; 305C047A020924A5 CRC64;

Query Match 61.7%; Score 2106.5; DB 13; Length 420;
Best Local Similarity 95.2%; Pred. No. 2.2e-163;
Matches 401; Conservative 13; Mismatches 6; Indels 1; Gaps 1;

QY 228 SOHRYSTPHAFNTSPSSGSLSORQSTSTPNVHMVSTLPVDSRMIEDAIRSHSES 287
DB 1 SOHRYSTPHAFNTSPSSGSLSORQSTSTPNVHMVSTLPVDSRMIEDAIRSHSES 60
QY 288 ASPSALSSPNNLSPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGQRDSSYYWEIEAS 347
DB 61 ASPSALSSPNNLSPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGQRDSSYYWEIEAS 120
QY 348 EVMLSRIGSGSGFYVYKKGWGDVAVKILKVDPTPEQFAFRNEAVLKRTRHVNILL 407
DB 121 EVMLSRIGSGSGFYVYKKGWGDVAVKILKVDPTPEQFAFRNEAVLKRTRHVNILL 180
QY 408 FMGYMTKDNLAIYVTCWCEGSSLYKHLHVQETKFKFQMFQFLIDIAQTACQMDYLHAKNIHR 467
DB 181 FMGYMTKDNLAIYVTCWCEGSSLYKHLHVQETKFKFQMFQFLIDIAQTACQMDYLHAKNIHR 240
QY 468 DMKSNNIFLHEGLTVKIGDFGLATVKSRSWGSQVQEQPTGSLVWMAPEVIRMQDNNPFSF 527
DB 241 DMKSNNIFLHEGLTVKIGDFGLATVKSRSWGSQVQEQPTGSLVWMAPEVIRMQDNNPFSF 300
QY 528 QSDVSYGIVLYELMTGELPYSHINNRRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVAD 587
DB 301 QSDVSYGIVLYELMTGELPYSHINNRRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVAD 360
QY 588 CVKVKKEERPLFPQILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPV 647
DB 361 CLKKVREERPLFPQILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPV 419
QY 648 F 648
DB 420 F 420

RESULT 6
Q85632 PRELIMINARY; PRT; 506 AA.
AC Q85632; Q85633;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE GAG polyprotein [Contains: core protein(s) P24] (Fragment).
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Db 184 MDYLHAKNIHHRDKMNNIFLHGLTVKIGDFGLATVKSRSQSQVEQPTGSIILMAPE 243
QY 516 VIRMQDNPFQSDVSYSGIVLYELMTGELPYSHINNRDQIFVMVGRGYASPDLSKLYK 575
Db 244 VIRMQDNPFQSDVSYSGIVLYELMTGELPYSHINNRDQIFVMVGRGYASPDLSKLYK 303
QY 576 NCPKMKRLVADCKVKVKEERPLFPOLSILOHSLPKINRSASEPSLHRAHTEDIN 635
Db 304 NCPKMKRLVADCKVKVKEERPLFPOLSILOHSLPKINRSASEPSLHRAHTEDIN 363
QY 636 ACTLTTPSRPLPV 648
Db 364 SCTLTSTRPLPV 375

RESULT 10

QY6T3 PRELIMINARY; PRT; 651 AA.
AC QY6T3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE WUGSC:H_DJ0726N20.3 protein (Fragment).
GN WUGSC:H_DJ0726N20.3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Cordes M., Wohldman P., Pape K., Hotic M.;
RT "The sequence of Homo sapiens PAC clone RP4-726N20.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC006344; RAD43193.1; -;
DR HSSP; P04049; IFAR.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF02196; RBD; 1.
DR PRINTS; PR00008; DAGPEMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 651 AA; 73395 MW; CD2C25EFF7D3E98C CRC64;

Query Match 49.4%; Score 1685; DB 4; Length 651;
Best Local Similarity 54.8%; Pred. No. 1e-128;
Matches 356; Conservative 68; Mismatches 126; Indels 100; Gaps 14;

QY 88 VRGLOPECCAVF-----LLHEHKGKKARLDWNTDAA 119
Db 1 MRGLPECCAVYRQDGPSTNFHIFSMRYNIFFCNQERLVSTFFREKKPKICWDIDIS 60
QY 120 SLIGELQVDFLDHVPFTTHNFARKTLFLKACDICORFLNGLFRQCOTCGYKPHGCHSTK 179
Db 61 WLTGELHVEVLENVPLTTHNFVAKTFTFLAFCDFCRKLLFGQFCQTCGKYPHQRCSST 120
QY 180 VPTWCVDKSNIRQLLFPNSIGSGVP-----ALPSLTWRWRRESVSRP--VS 227
Db 121 VPLMCVNYDQD--LLFVSKFEFHHPIQDEASLAETALTSGPSAPASDSIGPQIUTS 178
QY 228 SQHRYSTPHAFTEFTSSPSSSGSLSQRQSTSTNVHMVSTTLVPVDSRMIDAIRSHS-- 285
Db 179 PPSKSIPIQPFPRPADEHNFQQRDRSSAANVH-INTIEPVN---IDDLRDOGFR 234
QY 286 -----ESAPSP-ALSSSPNNL-----SPTGWSQ----- 307
Db 235 GDGAPLNQLMRCLRKYSRTSPLLHSVPSEIVDFEPGPVFRGTTGLSATPPASLPGS 294
QY 308 -----PKTPVPAQRERAPVSGTQENKIRPGORDSSYYWETEASEVMLSTRIGSGSF 360
Db 295 LTNVKALOKSPG-QREKSSSSSEDRNMKTILGRDSSDWEIPDQGITVQGRIIGSGSF 353
QY 361 GTVYKGWHDVAVYKILKWDPTPEQFAERNEVAVLRKTRHVNILLFMGYMTKDNLAIY 420
Db 354 GTVYKGWHDVAVYKMLNVTAFTPQQLQAFKNEVGLKTRHVNILLFMGYSTKPLAIY 413
QY 421 TQWCEGSSLYKHLHVQETKFFOMFOLIDIAQTACGMDYLHAKNIIHRDMKSNNTFLHEGL 480
Db 414 TQWCEGSSLYKHLHIIETKFEIKLIDIAQTACGMDYLHAKSIHRDLAKSNNTFLHEDL 473
QY 481 TVKIGDFGLATVKSRSQSQVEQPTGSIILMAPEVIRMODNPNFQSDVSYSGIVLYE 540
Db 474 TVKIGDFGLATVKSRSQSQVEQPTGSIILMAPEVIRMODNPNFQSDVSYSGIVLYE 533
QY 541 LMTGELPYSHINNRDQIFVMVGRGYASPDLSKLYKNCPKMKRLVADCKVKVKEERPLFP 600
Db 534 LMTGELPYSHINNRDQIFVMVGRGYASPDLSKLYKNCPKMKRLVADCKVKVKEERPLFP 593
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAA-HTEDIN--ACTLTTPSRPLPV 647
Db 594 QILASIELLAKSLPKIHRSAEPLNRAGFTQEDFSLYAC---ASPKTPI 640

RESULT 11

Q85453 PRELIMINARY; PRT; 359 AA.
AC Q85453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 3611 raf gene (Fragment).
OS Murine sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
OX NCBI_TaxID=11802;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84121298; PubMed=6320371;
RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
RT "A common onc gene sequence transduced by avian carcinoma virus MH2 and by murine sarcoma virus 3611.";
RL Science 223:813-816(1984).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; K02084; AAA46576.1; -;
DR HSSP; P12931; IFMK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003036; Gag_p30.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02093; Gag_p30; 1.
DR Pfam; PF00069; pkinase; 1.

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DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 359 AA; 40935 MW; 586C615C331570D CRC64;

Query Match 49.1%; Score 1675; DB 15; Length 359;
Best Local Similarity 89.8%; Pred. No. 2.7e-122;
Matches 325; Conservative 11; Mismatches 22; Indels 4; Gaps 3;

QY 288 ASPSALSSPNLSPGWSQKPTVPVPAQRERAPVS-GTQENKIRPRQRDSSYYWETEA 346
D 1 AKVKGITQGPNE-SFSAFLERLK--EAYRYTPYDPGTQENKIRPRQRDSSYYWKEA 57
QY 347 SEVMLSTRIGSGSGFTYVKGKHWGDAVKILKVVDPTPEQQAQFNEVAVLRKTRHVNIL 406
D 1 AKVKGITQGPNE-SFSAFLERLK--EAYRYTPYDPGTQENKIRPRQRDSSYYWKEA 57
QY 58 SEVMLSTRIGSGSGFTYVKGKHWGDAVKILKVVDPTPEQQAQFNEVAVLRKTRHVNIL 117
QY 407 LFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFOLIDIAQTAQGM DYLAHAKNIIH 466
D 1 AKVKGITQGPNE-SFSAFLERLK--EAYRYTPYDPGTQENKIRPRQRDSSYYWKEA 57
QY 118 LFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFOLIDIAQTAQGM DYLAHAKNIIH 177
QY 467 RDMKNNIFLHGLTVKIGDFGLATVKSRSQSQVEQPTGSLVWMAPEVIRMQDNNPFS 526
D 1 AKVKGITQGPNE-SFSAFLERLK--EAYRYTPYDPGTQENKIRPRQRDSSYYWKEA 57
QY 178 RDMKNNIFLHGLTVKIGDFGLATVKSRSQSQVEQPTGSLVWMAPEVIRMQDNNPFS 237
QY 527 FOSDYSYGVIVLYELMTGELPYSHNNRDQIIFWVGRCYASPDLSKLYKNCPCRAKRLVA 586
D 1 AKVKGITQGPNE-SFSAFLERLK--EAYRYTPYDPGTQENKIRPRQRDSSYYWKEA 57
QY 238 FOSDYSYGVIVLYELMTGELPYSHNNRDQIIFWVGRCYASPDLSKLYKNCPCRAKRLVA 297
QY 587 DCVKVKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLP 646
D 1 AKVKGITQGPNE-SFSAFLERLK--EAYRYTPYDPGTQENKIRPRQRDSSYYWKEA 57
QY 298 DCVKVKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLP 357
QY 647 VF 648
D 1 AKVKGITQGPNE-SFSAFLERLK--EAYRYTPYDPGTQENKIRPRQRDSSYYWKEA 57
D 358 VF 359

RESULT 12
QY 3636 PRELIMINARY; PRT; 308 AA.
AC 090336
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 6430402F14Rik protein (Fragment).
GN RAF1 OR 6430402F14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=OLFACTORY BRAIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL; AK018272; BAB31142.1; -.
DR HSP; P12931; IFMK.
DR MGD; MGI:97847; Raf1.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
FT NON_TER 1
SQ SEQUENCE 308 AA; 35058 MW; F87DD6ABE27600BB CRC64;

Query Match 46.2%; Score 1577; DB 11; Length 308;
Best Local Similarity 97.7%; Pred. No. 2.1e-120;
Matches 301; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 341 YWEIASEVMSLSTRIGSGFTYVKGKHWGDAVKILKVVDPTPEQQAQFNEVAVLRKT 400
D 1 YWEIASEVMSLSTRIGSGFTYVKGKHWGDAVKILKVVDPTPEQQAQFNEVAVLRKT 60
QY 401 RHVNILFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFOLIDIAQTAQGM DYLAH 460
D 1 RHVNILFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFOLIDIAQTAQGM DYLAH 120
QY 461 AKNIIHRDMKNNIFLHGLTVKIGDFGLATVKSRSQSQVEQPTGSLVWMAPEVIRMQ 520
D 1 AKNIIHRDMKNNIFLHGLTVKIGDFGLATVKSRSQSQVEQPTGSLVWMAPEVIRMQ 180
QY 121 AKNIIHRDMKNNIFLHGLTVKIGDFGLATVKSRSQSQVEQPTGSLVWMAPEVIRMQ 580
D 1 AKNIIHRDMKNNIFLHGLTVKIGDFGLATVKSRSQSQVEQPTGSLVWMAPEVIRMQ 240
QY 521 DNNPFSQSDYSYGVIVLYELMTGELPYSHNNRDQIIFWVGRCYASPDLSKLYKNCPCRA 580
D 1 DNNPFSQSDYSYGVIVLYELMTGELPYSHNNRDQIIFWVGRCYASPDLSKLYKNCPCRA 240
QY 581 MKRLVADCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLT 640
D 1 MKRLVADCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLT 300
QY 241 MKRLVADCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLT 300
QY 641 TSPRLPVF 648
D 1 TSPRLPVF 308
D 301 TSPRLPVF 308

RESULT 13
QY 019055 PRELIMINARY; PRT; 301 AA.
AC 019055
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-RAF homolog (Fragment).
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Mandiyan S., Schumacher C., Cioffi C., Sharif H., Yuryev A., Lappe R.,
RA Monia B., Hanson S., Goff S., Wennogle L. P.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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DR EMBL: AF006463; AAB63196.1; -.
DR HSSP: P12931; IFMK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00221; STYKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Serine/threonine-protein kinase.
KW NON_TER 1
FT SEQUENCE 301 AA; 34230 MW; 3512983ADP5D1A3B CRC64;

Query Match 46.1%; Score 1573; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 4.4e-120; Indels 0; Gaps 0;
Matches 301; Conservative 0; Mismatches 0;

QY 348 EYMLSTRIGSGSGFTYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNIL 407
Db 1 EYMLSTRIGSGSGFTYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNIL 60

QY 408 FMGYTKDNLAIYVQWCEGSSLYKHLHVQETKFMFQQLIDIAQTAAQMDYLHAKNIHR 467
Db 61 FMGYTKDNLAIYVQWCEGSSLYKHLHVQETKFMFQQLIDIAQTAAQMDYLHAKNIHR 120

QY 468 DMKSNNIFLHEGLTVKIGDFGLATVKRWSGSGQVEQPTGSLVWMAPEVIRMODNPPSF 527
Db 121 DMKSNNIFLHEGLTVKIGDFGLATVKRWSGSGQVEQPTGSLVWMAPEVIRMODNPPSF 180

QY 528 QSDVSYGIVLYELMTGELPYSHINNNDQIIFWVGRGYASPDLSKLYKNCPRAMKRLVAD 587
Db 181 QSDVSYGIVLYELMTGELPYSHINNNDQIIFWVGRGYASPDLSKLYKNCPRAMKRLVAD 240

QY 588 CVKVKVEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPV 647
Db 241 CVKVKVEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPV 300

QY 648 F 648
Db 301 F 301

RESULT 14
Q90458
ID Q90458 PRELIMINARY; PRT; 307 AA.
AC Q90458;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE C-raf protein (Fragment).
GN CRAF OR C-RAF.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Danio J.L.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: X81128; CAA57035.1; -.
DR HSSP: P12931; IFMK.
DR ZFIN: ZDB-GENE-990415-41; craf.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
```

```
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00221; STYKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 307 AA; 34871 MW; 588E3F416F8CB332 CRC64;

Query Match 41.0%; Score 1398.5; DB 13; Length 307;
Best Local Similarity 88.1%; Pred. No. 7.7e-106;
Matches 266; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 347 SEVMLSTRIGSGSGFTYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNIL 406
Db 7 NEVLLSRIGSGSGFTYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNIL 66

QY 407 LFMGYTKDNLAIYVQWCEGSSLYKHLHVQETKFMFQQLIDIAQTAAQMDYLHAKNIHR 466
Db 67 LFMGYTKDNLAIYVQWCEGSSLYKHLHVQETKFMFQQLIDIAQTAAQMDYLHAKNIHR 126

QY 467 DMKSNNIFLHEGLTVKIGDFGLATVKRWSGSGQVEQPTGSLVWMAPEVIRMODNPPSF 526
Db 127 DMKSNNIFLHEGLTVKIGDFGLATVKRWSGSGQVEQPTGSLVWMAPEVIRMODNPPSF 186

QY 527 FQSDVSYGIVLYELMTGELPYSHINNNDQIIFWVGRGYASPDLSKLYKNCPRAMKRLVA 586
Db 187 FQSDVSYGIVLYELMTGELPYSHINNNDQIIFWVGRGYASPDLSKLYKNCPRAMKRLVA 246

QY 587 DCVKVKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRP 646
Db 247 DCVKVKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRP 305

QY 647 VF 648
Db 306 VF 307

RESULT 15
Q9DBE2
ID Q9DBE2 PRELIMINARY; PRT; 285 AA.
AC Q9DBE2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein kinase raf 1 (Fragment).
GN CRAF.
OS Seriola quinqueradiata (Five-ray yellowtail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Carangidae; Seriola.
OX NCBI_TaxID=8161;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Doi M., Abe S.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Gray T.A., Azama K., Whitmore K.L., Min A., Abe S., Nicholls R.D.;
RT "A conserved gene antisense to the proto-oncogene c-RAF encodes a
RT multi-zinc-finger protein, MAKORIN2."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB049965; BAB18860.1; -.
DR HSSP: P12931; IFMK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
```

```
DR ProDom: PD000001: Euk_pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 285 AA; 32519 MW; 99A692B08A9D4668 CRC64;

Query Match          40.8%; Score 1391.5; DB 13; Length 285;
Best Local Similarity 92.3%; Pred. No. 2.6e-105;
Matches 264; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 363 VYKGKWHGDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYMTKONLAIVTQ 422
Db      1 VYKGKWHGDVAVKILKVTDPTPEQFAFRNEVAVLRKTRHVNILLFMGYMTKONLAIVTQ 60

QY 423 WCEGSSLYKHLHVQETKQFQQLIDIAQRTAQGMDYLHAKNIIHRDMKSNNIFLHEGLTV 482
Db      61 WCEGSSLYKHLHVLETNFKMIQLIDIAQRTAQGMDYLHAKNIIHRDMKSNNIFLHEGLTV 120

QY 483 KIGDFGLATVKRWGSGOQVPTGSGVLWMAPEVIRMQDNNPFSQSDVYSYGIVLYELM 542
Db      121 KIGDFGLATVKRWGSGHQPSPGSLWMAPEVIRMQDNNPYSFQSDVYSYGIVLYELM 180

QY 543 TGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFPQI 602
Db      181 TGELPYSQIANRDQIIFMVGRGYLSPDLSKLYKNCPKAMKRLVADCIKSKDERPLFPQI 240

QY 603 LSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648
Db      241 LSSIELLOHALPKINRSASEPSLHRAAHTEDINACTLT-TSTRLPVF 285
```

Search completed: July 9, 2003, 09:46:14
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:43:12 ; Search time 22 Seconds
(without alignments)
2831.596 Million cell updates/sec

Title: US-09-637-302C-2
Perfect score: 3413
Sequence: 1 MEHIQAWKTIISNGFGKDA.....AHTEDINACTLTSPRLPVF 648

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3413	100.0	648	1	TVHUF6
2	3349	98.1	648	1	TVTRRF
3	3249.5	95.2	647	1	S00644
4	2885	84.5	638	1	TVXLRP
5	1927	56.5	602	1	TVTRFR
6	1891.5	55.4	604	1	S00726
7	1889.5	55.4	606	1	TVHUAF
8	1888.5	55.3	380	1	TVFYVM
9	1825	53.5	765	1	TVHUBF
10	1814	53.1	806	1	JN0612
11	1814	53.1	807	1	I51153
12	1654	48.5	333	1	TVWVF6
13	1409.5	41.3	437	1	TVMSRF
14	1398.5	41.0	307	2	S47244
15	1365	40.0	781	1	TVTFDF
16	1338	39.2	1079	1	TVFVMI
17	1336	39.1	450	1	TVFVMR
18	1277	37.4	338	1	TVMSBF
19	1121.5	32.9	813	1	S33261
20	569.5	16.7	1003	2	T13856
21	493.5	14.5	553	2	T04683
22	491.5	14.4	546	2	D84555
23	466.5	13.7	1030	2	F96763
24	455.5	13.3	821	2	T48400
25	440	12.9	899	2	T07406
26	426	12.5	406	2	T52626
27	421	12.3	412	2	T10671
28	421	12.3	963	2	T09911
29	412.5	12.1	568	1	TVFVSI

30	409.5	12.0	736	2	T05137	protein kinase hom
31	407	11.9	528	1	TVFVG9	protein-tyrosine k
32	407	11.9	738	2	F96701	hypothetical prote
33	406	11.9	542	2	A49114	protein-tyrosine k
34	404	11.8	505	2	I38396	protein-tyrosine k
35	404	11.8	541	1	TVCHYS	protein-tyrosine k
36	403	11.8	537	1	A43806	protein-tyrosine k
37	403	11.8	537	1	TVHUSY	protein-tyrosine k
38	403	11.8	1015	2	T00726	probable serine/thr
39	402	11.8	537	2	I51592	protein-tyrosine k
40	401.5	11.8	505	1	S24550	protein-tyrosine k
41	401	11.7	544	2	I51593	protein-tyrosine k
42	400	11.7	982	2	T06576	probable protein k
43	399.5	11.7	509	2	T04688	hypothetical prote
44	398	11.7	475	2	T12955	probable protein k
45	398	11.7	545	2	T05675	hypothetical prote

RESULT 1
TVHUF6
protein kinase raf-1 (EC 2.7.1.-) - human
N:Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene pr
N:Contains: protein kinase (EC 2.7.1.37)
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 11-Jun-1999
C:Accession: A00637; I57580
R:Bonner, T.I.; Oppermann, H.; Seeburg, P.; Kerby, S.B.; Gunnell, M.A.; Young, A.C.;
Nucleic Acids Res. 14, 1009-1015, 1986
A:Title: The complete coding sequence of the human raf oncogene and the corresponding
A:Reference number: A00637; MUID:86120351; PMID:3003687
A:Accession: A00637
A:Molecule type: mRNA
A:Residues: 1-648 <BON1>
A:Cross-references: GB:X03484; NID:g35841; PIDN:CAA37204.1; PID:g35842
R:Bonner, T.I.; Kerby, S.B.; Suttrave, P.; Gunnell, M.A.; Mark, G.; Rapp, U.R.
Mol. Cell. Biol. 5, 1400-1407, 1985
A:Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A:Reference number: I57580; MUID:85295973; PMID:2993863
A:Accession: I57580
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 228-239, 'L', '241-541, 'I', '543-648 <BON2>
A:Cross-references: GB:L00212; NID:g190837; PIDN:AAA60247.1; PID:g496091
R:Morrison, D.K.; Heidecker, G.; Rapp, U.R.; Copeland, T.D.
J. Biol. Chem. 268, 17309-17316, 1993
A:Title: Identification of the major phosphorylation sites of the Raf-1 kinase.
A:Reference number: A43089; MUID:93352516; PMID:8349614
A:Contents: annotation; phosphorylation sites
A:Note: expression is ubiquitous in mammalian tissues that have been studied
C:Comment: After phosphorylation and activation by protein kinase C and other kinases
C:Genetics:
A:Gene: GDB:RAF1
A:Cross-references: GDB:I19546; OMIM:164760
A:Map position: 3p25-3p25
A:Introns: 278/3; 288/1; 330/3; 370/1; 398/2; 457/2; 473/1; 512/3; 556/3; 601/3
A:Note: the list of introns is incomplete
C:Function:
A:Description: catalyzes the formation of specific peptidyl-threonine-phosphate and p
A:Pathway: MAP kinase cascade
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:347-613/Domain: protein kinase A-raf binding motif
F:355-363/Region: protein kinase A-raf binding motif
F:43, 621/Binding site: phosphate (Ser) (covalent) #status experimental
F:139,165,168,184/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:152,155,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experime
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status exper
F:375/Active site: Lys #status predicted

ALIGNMENTS

F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 100.0%; Score 3413; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.8e-170;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTIISNGFGKDAVFDGSSCISPTIVQFGYORRASDGLTDPKTSNTIRV 60
DB 1 MEHIQAWKTIISNGFGKDAVFDGSSCISPTIVQFGYORRASDGLTDPKTSNTIRV 60

QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120

QY 121 LIGELQVDFLDHVPVLTTHNFARKTEFLKLAFCIDICQKFLNGFRCTOCYKPFHCSTKV 180
DB 121 LIGELQVDFLDHVPVLTTHNFARKTEFLKLAFCIDICQKFLNGFRCTOCYKPFHCSTKV 180

QY 181 PTMCVDSNIRQLLPNSTIGDVGVPALPSLTMRMRRESVSRMPVSSOHRYSTPHATF 240
DB 181 PTMCVDSNIRQLLPNSTIGDVGVPALPSLTMRMRRESVSRMPVSSOHRYSTPHATF 240

QY 241 NTSSPSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
DB 241 NTSSPSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300

QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPGQRDSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPGQRDSYYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKKGWGDVAVKILKVVDPTEPQFAFRNEVAVLRTRHVNILLFMGYMTKDNLAIV 420
DB 361 GTVYKKGWGDVAVKILKVVDPTEPQFAFRNEVAVLRTRHVNILLFMGYMTKDNLAIV 420

QY 421 TOWCEGSSLYKHLHVQETKQFQMLDIAQTAQGMIDYLAHAKNIIHRDMKSNIFLHEGL 480
DB 421 TOWCEGSSLYKHLHVQETKQFQMLDIAQTAQGMIDYLAHAKNIIHRDMKSNIFLHEGL 480

QY 481 TVKIGDFGLATVKSRSWSGQVEQPTGVLWMAPEVIRMQDNNPFSQSDVYSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRSWSGQVEQPTGVLWMAPEVIRMQDNNPFSQSDVYSYGIVLYE 540

QY 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKKYKERRPLFP 600
DB 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKKYKERRPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 2
TVTRF
protein kinase raf-1 (EC 2.7.1.1) - rat
N:Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C:Accession: A26126
R:Shikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A:Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein.
A:Reference number: A26126; MUID:87172791; PMID:3550433
A:Accession: A26126
A:Molecule type: mRNA
A:Residues: 1-648 <ISH>
A:Cross-references: GB:M15427; NID:g206544; PIDN:AAA42001.1; PID:g206545
C:Genetics:
A:Gene: raf
C:Function:
A:Description: signal transduction between cell membrane and nucleus; after phosphorylat
A:Pathway: Map kinase cascade
A>Note: expression is ubiquitous in mammalian tissues that have been studied
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot

C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:347-613/Domain: protein kinase homology <KIN>
F:355-363/Region: protein kinase ATP-binding motif
F:43-621/Binding site: phosphate (Ser) (covalent) #status predicted
F:139,165,168,184/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:152,135,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F:375/Active site: Lys #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predi

Query Match 98.1%; Score 3349; DB 1; Length 648;
Best Local Similarity 98.3%; Pred. No. 5.9e-167;
Matches 637; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 MEHIQAWKTIISNGFGKDAVFDGSSCISPTIVQFGYORRASDGLTDPKTSNTIRV 60
DB 1 MEHIQAWKTIISNGFGKDAVFDGSSCISPTIVQFGYORRASDGLTDPKTSNTIRV 60

QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120

QY 121 LIGELQVDFLDHVPVLTTHNFARKTEFLKLAFCIDICQKFLNGFRCTOCYKPFHCSTKV 180
DB 121 LIGELQVDFLDHVPVLTTHNFARKTEFLKLAFCIDICQKFLNGFRCTOCYKPFHCSTKV 180

QY 181 PTMCVDSNIRQLLPNSTIGDVGVPALPSLTMRMRRESVSRMPVSSOHRYSTPHATF 240
DB 181 PTMCVDSNIRQLLPNSTIGDVGVPALPSLTMRMRRESVSRMPVSSOHRYSTPHATF 240

QY 241 NTSSPSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
DB 241 NTSSPSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300

QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPGQRDSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPGQRDSYYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKKGWGDVAVKILKVVDPTEPQFAFRNEVAVLRTRHVNILLFMGYMTKDNLAIV 420
DB 361 GTVYKKGWGDVAVKILKVVDPTEPQFAFRNEVAVLRTRHVNILLFMGYMTKDNLAIV 420

QY 421 TOWCEGSSLYKHLHVQETKQFQMLDIAQTAQGMIDYLAHAKNIIHRDMKSNIFLHEGL 480
DB 421 TOWCEGSSLYKHLHVQETKQFQMLDIAQTAQGMIDYLAHAKNIIHRDMKSNIFLHEGL 480

QY 481 TVKIGDFGLATVKSRSWSGQVEQPTGVLWMAPEVIRMQDNNPFSQSDVYSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRSWSGQVEQPTGVLWMAPEVIRMQDNNPFSQSDVYSYGIVLYE 540

QY 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKKYKERRPLFP 600
DB 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKKYKERRPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 3
S00644
protein kinase raf-1 (EC 2.7.1.1) - chicken
N:Alternate names: kinase-related transforming protein raf-1; mht/raf; protein kinase
C:Species: Gallus gallus (chicken)
C:Date: 18-Oct-1989 #sequence_revision 23-Aug-1996 #text_change 11-Jun-1999
C:Accession: S00644; I50380; I50381
R:Koenen, M.; Sippl, A.E.; Trachmann, C.; Blster, K.
Oncogene 2, 179-185, 1988
A:Title: Primary structure of the chicken c-mil protein: identification of domains sh
A:Reference number: S00644; MUID:98217299; PMID:3285296

A:Accession: S00644
A:Molecule type: mRNA
A:Residues: 1-647 <KOE>
A:Cross-references: EMBL:X07017; NID:963232; PIDN:CAA30069.1; PID:g63233
R:Flordellia, C.S.; Kan, N.C.; Lautenberger, J.A.; Samuel, K.P.; Garon, C.F.; Papas, T.S.
Virology 141, 267-274, 1985
A:Title: Analysis of the cellular proto-oncogene mht/raf: Relationship to the 5' sequenc
A:Reference number: 150380; MUID:86098644; PMID:3002017
A:Accession: 150380
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 230-330 <FLO>
A:Cross-references: GB:K03048; NID:g212306; PIDN:AAA48951.1; PID:g212308
R:Jansen, H.W.; Bister, K.
Virology 143, 359-367, 1985
A:Title: Nucleotide sequence analysis of the chicken gene c-mil, the progenitor of the
A:Reference number: 150381; MUID:86045899; PMID:2998016
A:Accession: 150381
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 228-548, 'F', 550-647 <JAN>
A:Cross-references: GB:K03269; NID:g212319; PIDN:AAA48952.1; PID:g212321
C:Genetics:
A:Introns: 278/3; 288/1; 330/3; 370/1; 398/2; 457/2; 473/1; 512/3; 556/3; 601/3
A:Note: the list of introns may be incomplete
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: MAP kinase cascade
A:Note: after phosphorylation and activation by protein kinase C, phosphorylates and act
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:347-613/Domain: protein kinase homology <KIN>
F:355-363/Region: protein kinase ATP-binding motif
F:43-621/Binding site: phosphate (Ser) (covalent) #status predicted
F:139,165,168,184/Binding site: zinc (His, Cys, Cys) #status predicted
F:154,155,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
F:375,393,468,470/Active site: Lys, Glu, Asp, Lys #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 95.28; Score 3249.5; DB 1; Length 647;
Best Local Similarity 94.68; Pred. No. 8.7e-162;
Matches 613; Conservative 20; Mismatches 14; Indels 1; Gaps 1;

QY 1 MEHQGAWKTSNGFGFKDAVFGSGCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
DB 1 MEHQGAWKTSNGFGKDSVDFGPNCSPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60

QY 61 FLPNKQRTVNVNRNGMSLHDLCKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVNVNRNGMTLHDLCKALKVRGLQPECCAVFRLVTEPKGKVRLDWNTDAAS 120

QY 121 LIGELQVDFLDHVPDLTHNFARTFLKLAFCDCIQKFLNGFCQFCGKFKFHCSTKV 180
DB 121 LIGELQVDFLDHVPDLTHNFARTFLKLAFCDCIQKFLNGFCQFCGKFKFHCSTKV 180

QY 181 PTMCVDWNIKQLLLFPNSTIGDSVPALPSLTMRKRRESVRMPVSSQHRYSPPHFTF 240
DB 181 PTMCVDWNIKQLLLFPNSNISDSGVPALPLTMRKRRESVSRIPVSSQHRYSPPHFTF 240

QY 241 NTSPPSSGSLSQRSQRTSTPNVHMVSTLTPVDSRMIEDAIRHSESASPSALSSPNNL 300
DB 241 NTSPPSSGTLSQRSQRTSTPNVHMVSTLTPVDSRIIEDAIRHSESASPSALSSPNNM 300

QY 301 SPTGWSQKTPVPAQRERAPVSGTOEKNKIRPGORDSSYYWEATESEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPGNTQEKNKIRPGORDSSYYWEATESEVMLSTRIGSGSF 360

QY 361 GTVYKGKWHGDVAVKILKVDPTPEQQAERNEAVLRKTRHVILLFMGYMTKDLNLAIV 420
DB 361 GTVYKGKWHGDVAVKILKVDPTPEQQAERNEAVLRKTRHVILLFMGYMTKDLNLAIV 420

QY 421 TQWCESSLYKHLHVQETKQFMQLIDIAROTQAGMDYLHAKNIIHRDMKSNINFLHBEGL 480
DB 421 TQWCESSLYKHLHVQETKQFMQLIDIAROTQAGMDYLHAKNIIHRDMKSNINFLHBEGL 480

QY 481 TVKIGDFGLATVKSRWSQSQVQEQPTGTVLWMAPEVIRMQDNPNPFSQSDVSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRWSQSQVQEQPTGTVLWMAPEVIRMQDNPNPFSQSDVSYGIVLYE 540

QY 541 LMTGELPYSHINNROQIIFWVGGRGASPDLSKLYKNCPKAMKRLVADCVKKVKEERPLFP 600
DB 541 LMTGELPYSHINNROQIIFWVGGRGASPDLSKLYKNCPKAMKRLVADCLKKVREERPLFP 600

QY 601 QILSSTIELQHSPLPKINRSASPSLHRAAHTEDINACTLTTPSRPLPVF 648
DB 601 QILSSTIELQHSPLPKINRSASEPSLHRASHTEDINACTLTTPSRPLPVF 647

RESULT 4
TVXLRP
protein kinase raf-1 (BC 2.7.1.-) - African clawed frog
N:Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene pr
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 11-Jun-1999
C:Accession: S01930; 151254
R:Le Guellec, R.; Le Guellec, K.; Paris, J.; Philippe, M.
Nucleic Acids Res. 16, 10357, 1988
A:Title: Nucleotide sequence of Xenopus C-raf coding region.
A:Reference number: S01930; MUID:89057471; PMID:3194203
A:Accession: S01930
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-638 <LEG>
A:Cross-references: EMBL:X12948; NID:g65027; PIDN:CAA31407.1; PID:g65028
R:Le Guellec, R.; Couturier, A.; Le Guellec, K.; Paris, J.; Le Fur, N.; Philippe, M.
Biol. Cell 72, 39-45, 1991
A:Title: Xenopus c-raf proto-oncogene: cloning and expression during oogenesis and ea
A:Reference number: 151254; MUID:92096753; PMID:1721855
A:Accession: 151254
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-308, 'R', 310-638 <LEX>
A:Cross-references: GB:S74063; NID:g241259; PIDN:AAB20707.1; PID:g241260
C:Genetics:
A:Gene: raf
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
A:Pathway: MAP kinase cascade
A:Note: after phosphorylation and activation by protein kinase C, phosphorylates and
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:138-183/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:338-604/Domain: protein kinase homology <KIN>
F:346-354/Region: protein kinase ATP-binding motif
F:43/Binding site: phosphate (Ser) (covalent) #status predicted
F:138,164,167,183/Binding site: zinc (His, Cys, Cys) #status predicted
F:151,154,172,175/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:257/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:266/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F:366,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted
F:490/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 84.5%; Score 2885; DB 1; Length 638;
Best Local Similarity 85.3%; Pred. No. 7.5e-143;
Matches 553; Conservative 35; Mismatches 50; Indels 10; Gaps 4;

QY 1 MEHQGAWKTSNGFGFKDAVFGSGCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
DB 1 MEHQGAWKTSNGFGFKESVFEGSGSCMPTIVHQFGYQRRASDDGKLTDPKSTNTIRV 60

QY 61 FLPNKQRTVNVNRNGMSLHDLCKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
DB 61 YLPNKQRTVNVNRNGMSLHDLCKALKVRGLQPECCAVFRLIQDPKG-KLRLDWNTDAAS 119

QY 121 LIGELQVDFLDVHPLTHNFARKTKLAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
DB 120 LVGAELQVDFLDVHPLTHNFARKTKLAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 179
QY 181 PTMCVDSNTRQLLLPNSNIGSGVPALPSLTMRRRESVSRMPVSSQHRVSTPHAFWF 240
DB 180 PTMCVDSNTRQLLLPNSNIGSGVTPSLTMRRIGESV-RIPVSSQORVSTPHPF 238
QY 241 NTSPSSSELSQORSTSTPNVHMVSTTLPLVDSRMIEDAIRSHSESASPSALSSSPNML 300
DB 239 STSPVSECSLSQORSTSTPNVHMVSTTMVDSRVIEDALRSHSE-----SGSPNML 291
QY 301 SPFGWSOPKTPVPAQRERAPVSTQKKNKTRPGQRDSSYWIIEASEVNLSTRIGSGSF 360
DB 292 SPTGWSNAKAPATHREKAASSTQKKNKTRARGQRDSSYWIIEASEVNLSTRIGSGSF 351
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQFOAFRNEVAVLRTRHVNILFNGYMTKDNLAIV 420
DB 352 GTVYKKGWHDVAVKILKVVDPTPEQFOAFRNEVAVLRTRHVNILFNGYMTKDNLAIV 411
QY 421 TOMCEGSSLYKHLHVQETKFMQFOLIDIAQTAGQMDYLHAKNIIHRDMKSNIFLHEGL 480
DB 412 TOMCEGSSLYKHLHVQETKFMQFOLIDIAQTAGQMDYLHAKNIIHRDMKSNIFLHEGL 471
QY 481 TVKIGDEGLATVKSRRSGSQOVPQPGSVLWMAPEVIRMQDNNPFSQSDVTSYGIVLYE 540
DB 472 TVKIGDEGLATVKSRRSGSQOVPQPGSVLWMAPEVIRMQDNNPFSQSDVTSYGIVLYE 531
QY 541 LMTGELPYSHINNRDQIIFMVGGRYASPDLSKLYKNCPRKMLVADCKVKKERPLFP 600
DB 532 LMTGELPYSHINNRDQIIFLGVGGVVPDLSKLYKNCPRKMLVADCKVKKERPLFP 591
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTITTS 648
DB 592 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTITTS 638

RESULT 5
TVTRRR
protein kinase (EC 2.7.1.37) raf - rat
N:Alternate names: Kinase-related transforming protein raf; raf proto-oncogene protein-s
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C:Accession: B26126
R:Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A:Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein.
A:Reference number: A26126; MUID:87172791; PMID:3550433
A:Accession: B26126
A:Molecule type: mRNA
A:Residues: 1-602 <ISH>
A:Cross-references: GB:M15428; NID:G206546; PIDN:AAA42002.1; PID:G206547
C:Genetics:
C:Superfamily: rat protein kinase raf; protein kinase homology
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine
F:301-567/Domain: protein kinase homology <kin>
F:309-317/Region: protein kinase ATP-binding motif
F:329/Active site: Lys #status predicted
F:453/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 56.5%; Score 1927; DB 1; Length 602;
Best Local Similarity 79.4%; Pred. No. 4.3e-93;
Matches 386; Conservative 22; Mismatches 54; Indels 24; Gaps 4;

QY 173 HECSTKVPMTCDVMSNIRQLLFPNSTIGD-----SGVPALPSLTMRRRESVS 222
DB 131 NERLSEVEYLEDYKRLNKLKESNTYKGEQLKLDELQASDV-----TVYRERLQ 186
QY 223 RMPVSSQHRVSTPHAFTHNTSPSSSELSQORSTSTPNVHMVSTTLPLVDSRMIEDAIR 282
DB 187 KELLHNONSW-----LNTLTKTKTDALLALGREGKNEILELKTCT---LENKKBDAIR 236

QY 283 SHSESASPSALSSSPNLSPTGWSOPKTPVPAQRERAPVSTQKKNKTRPGQRDSSYIW 342
DB 237 SHSESASPSALSSSPNLSPTGWSOPKTPVPAQRERAPVSTQKKNKTRPGQRDSSYIW 296
QY 343 ETEASEVNLSTRIGSGSFVYKKGWHDVAVKILKVVDPTPEQFOAFRNEVAVLRTRH 402
DB 297 ETEASEVNLSTRIGSGSFVYKKGWHDVAVKILKVVDPTPEQFOAFRNEVAVLRTRH 356
QY 403 VNILFNGYMTKDNLAIVTOMCEGSSLYKHLHVQETKFMQFOLIDIAQTAGQMDYLHAK 462
DB 357 VNILFNGYMTKDNLAIVTOMCEGSSLYKHLHVQETKFMQFOLIDIAQTAGQMDYLHAK 416
QY 463 NIIHRDMKSNIFLHEGLTVKIGDEGLATVKSRRSGSQOVPQPGSVLWMAPEVIRMQD 522
DB 417 NIIHRDMKSNIFLHEGLTVKIGDEGLATVKSRRSGSQOVPQPGSVLWMAPEVIRMQD 476
QY 523 NPFSQSDVTSYGIVLYELMTGELPYSHINNRDQIIFMVGGRYASPDLSKLYKNCPRK 582
DB 477 NPFSQSDVTSYGIVLYELMTGELPYSHINNRDQIIFMVGGRYASPDLSKLYKNCPRK 536
QY 583 RLVADCVKVKKEERLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTITTS 642
DB 537 RLVADCVKVKKEERLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTITTS 596
QY 643 PRLPVF 648
DB 597 PRLPVF 602

RESULT 6
S00726
protein kinase A-raf-1 (EC 2.7.1.1) - rat
N:Alternate names: A-raf-1 proto-oncogene protein-serine/threonine kinase; kinase-rel
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 23-Aug-1996 #text_change 11-Jun-1999
C:Accession: S00726
R:Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Oncogene Res. 1, 243-253, 1987
A:Title: The complete primary structure of the rat A-raf cDNA coding region: conserva
A:Reference number: S00726; MUID:88217324; PMID:3449797
A:Accession: S00726
A:Molecule type: mRNA
A:Residues: 1-604 <ISH>
A:Cross-references: EMBL:X06942; NID:G55756; PIDN:CAA30023.1; PID:G55757
C:Function:
A:Description: signal transduction between cell membrane and nucleus; after phosphory
A:Pathway: MAP kinase cascade
A>Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tiss
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:99-144/Domain: protein kinase C zinc-binding repeat homology <kin>
F:306-572/Domain: protein kinase homology <kin>
F:314-322/Region: protein kinase ATP-binding motif
F:99-125,128,144/Binding site: zinc (His, Cys, Cys) #status predicted
F:112,115,133,136/Binding site: zinc (Cys, His, His, Cys) #status predicted
F:214/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:223/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F:334/Active site: Lys #status predicted
F:580/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 55.4%; Score 1891.5; DB 1; Length 604;
Best Local Similarity 61.7%; Pred. No. 3e-91;
Matches 377; Conservative 76; Mismatches 125; Indels 33; Gaps 10;

QY 50 DPSTSTNTRVFLPNKORTVVVNRGMSLHDLCKALKVRLQPECCAVFRLHEHGKK 109
DB 13 EPSSAVGTAVKYLPNKORTVVVNRGMSLHDLCKALKVRLQPECCAVFRLHEHGKK 69
QY 110 ARLDWNTDAASLIGEEQLQVDFLDVHPLTHNFARKTKLAFCDICQKFLNGRCOTCG 169
DB 70 TVTAWDTAIPLDGEELIVELEDVPLTMHNFVRKTFVFLAFCDICQKFLNGRCOTCG 129

QY 170 YKFEHCSTKPTKVCVDWS-NIRQLLPNPTIGSDGVPALPSLTMRMRRESVSRMPVSS 228
Db 130 YKFEHCSSKPTKVCVDWSNRRQFYHSIQDLSSGS-----RQEVPSNLSVNE 178
QY 229 QHRYSTPHAFN-----FNTSSPSSSEGLSORQSTSTPNVHMVSTTLTPVDSRMIEDAIRS 283
Db 179 LITQGPSPFTQQDQEHFSPAPNPPLQIRSTSTPNVHMVSTTAPMDSSLMQFTQAS 238
QY 284 HSESA-----SPSALSSSPNNLSPTGWSQPKTPVPA-QRERAPVSGTOEKKIRPRGQ 335
Db 239 FSTDAAGRGDGPAG-SPSPASVS-SGRKSPHSKLPAEQREKSLA--DEKKVKNLGY 294
QY 336 RDSYVWEIEASEVWALSTRIGSGFGVYKKGWGDVAVKILKVVDPPTQFOAFRNEVA 395
Db 295 RDSGYVWPEVSEVQLKRIGTSGFGVFRGRWGDVAVKYLKVAQPTAEQAQAFKNEQ 354
QY 396 VLKTRHVNILLFMGYMTKDLAIWTCWCESSLYKHLVQETKQFQFOLIDTARQTAQ 455
Db 355 VLKTRHVNILLFMGYMTKQFALITQWCESSLYHHLVADTRFDMVQLIDVARQTAQ 414
QY 456 MDYLHAKNIIHRDMKSNFIHLEGLTVKIGDFGLATVKSWSGQQVQPTGSLYVMAPE 515
Db 415 MDYLHAKNIIHRDLKSNFIHLEGLTVKIGDFGLATVKTWSGAQPLEQPSGSLYVMAAE 474
QY 516 VIRMODNPFQSDVTSYGIVLYELMTGELPYSHINNRDQIIPVGRGVASPDLSLYK 575
Db 475 VIRMODNPFQSDVTAIGVLYELMTGSLPYSHIGSDQIIPVGRGVASPDLSLYK 534
QY 576 NCPKAMKRLVADCVKVKKEERPLFPQILSTELQHSPLKPNRSASEPSLHRAHTEIN 635
Db 535 NCPKAMRLLTDLKLFQREERPLFPQILATIELLQSLPKIERSASEPSLHR-TQADELP 593
QY 636 ACTLTSPRLP 646
Db 594 ACLLSAARLVP 604

RESULT 7

TVHDAF
N: protein kinase A-raf-1 (EC 2.7.1.1) - human
A: Alternate names: A-raf-1 proto-oncogene protein-serine/threonine kinase; kinase-related
C: Species: Homo sapiens (man)
C: Date: 31-Dec-1988 sequence-revision 14-Jul-1994 #text_change 16-Jun-2000
A: Accession: A53026; A26439; A23541
R: Lee, J.E.; Beck, T.W.; Brennscheidt, U.; DeGennaro, L.J.; Rapp, U.R.
Genomics 20, 43-55, 1994
A: Title: The complete sequence and promoter activity of the human A-raf-1 gene (ARAF1).
A: Reference number: A53026; MUID: 94292185; PMID: 8020955
A: Accession: A53026
A: Status: not compared with conceptual translation
A: Molecule type: DNA
A: Residues: 1-606 <LEE>
A: Cross-references: GB:L24038; NID:g508473; PIDN:AAA65219.1; PID:g780127
R: Beck, T.W.; Huleihel, M.; Gannell, M.; Bonner, T.I.; Rapp, U.R.
Nucleic Acids Res. 15, 595-609, 1987
A: Title: The complete coding sequence of the human A-raf-1 oncogene and transforming act
A: Reference number: A26439; MUID: 87146380; PMID: 3029685
A: Accession: A26439
A: Molecule type: mRNA
A: Residues: 1-297, 'X', 299-606 <BEC>
A: Cross-references: EMBL:X04790; NID:g28820; PIDN:CAA28476.1; PID:g1340152
R: Mark, G.E.; Sealey, T.W.; Shows, T.B.; Mountz, J.D.
Proc. Natl. Acad. Sci. U.S.A. 83, 6312-6316, 1986
A: Title: pKs, a raf-related sequence in humans.
A: Reference number: A23541; MUID: 86313571; PMID: 3529082
A: Accession: A23541
A: Molecule type: mRNA
A: Residues: 292-367, 'P', 369-377, 'V', 379-468, 'P', 470-477, 'T', 479-589 <MAR>
A: Cross-references: GB:M13829; NID:g189999; PIDN:AA08754.1; PID:g987023
C: Genetics:
A: Gene: GDB:ARAF1
A: Cross-references: GDB:119004; OMIM:311010
A: Map position: Xp11.3-Xp11.23

A: Introns: 32/3; 67/2; 101/3; 153/2; 186/2; 230/3; 240/1; 288/3; 356/2; 415/2; 431/1;
C: Function:
A: Description: signal transduction between cell membrane and nucleus; after phosphory
A: Pathway: MAP kinase cascade
A: Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tiss
C: Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C: Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F: 99-144/Domain: protein kinase C zinc-binding repeat homology <K2N>
F: 308-574/Domain: protein kinase homology <KIN>
F: 316-324/Region: protein kinase ATP-binding motif
F: 99,125,128,144/Binding site: zinc (His, Cys, Cys) #status predicted
F: 112,115,133,136/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F: 214/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F: 223/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F: 336/Active site: Lys #status predicted
F: 582/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 55.4%; Score 1889.5; DB 1; Length 606;
Best Local Similarity 61.9%; Pred. No. 3.8e-91;
Matches 376; Conservative 76; Mismatches 132; Indels 23; Gaps 9;

QY 50 DPSTSTNTIRVFLPNKORTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLHEHKGK 109
Db 13 EPRAGTVKVIYLPNQRVTVVDRGMSVDSLDKALKVRGLNODCCVYRLI---KGRK 69
QY 110 ARLDWNTDAASLIGEEQLVDLHDVPLTTHNFARKTFLKLAFCIDICQKFLNGFCQTCG 169
Db 70 TVTAWDTATADLGEELIVELEVDVPLTMHNFVKRTFFSLAFCDCLFLKHGFCQTCG 129
QY 170 YKFEHCSTKPTKVCVDWSNIRQLLPNPTIGSDGVPALPSLTMRMRRESVSRMPVSS 228
Db 130 YKFEHCSSKPTKVCVDWSNRRQFYHSIQDLSSGS-----RQEVPSNLSVNE 187
QY 229 QHRYSTPHAFN-----FNTSSPSSSEGLSORQSTSTPNVHMVSTTLTPVDSRMIE-----DA 280
Db 188 RTQCHDPEHFPF-----PAPANAPLQIRSTSTPNVHMVSTTAPMDSSLMQFTQAS 243
QY 281 IRSHSEASPSALSSSPNNLSPTGWSQPKTPVPA-QRERAPVSGTOEKKIRPRGQDSS 339
Db 244 AGSRGSGDGTGRGSPSPASVS-SGRKSPHSKLPAEQREKSLA--DDKKVKNLGYRDSG 300
QY 340 YKFEIEASEVWALSTRIGSGFGVYKKGWGDVAVKILKVVDPPTQFOAFRNEVAVLK 399
Db 301 YKFEVPEVSEVQLKRIGTSGFGVFRGRWGDVAVKYLKVAQPTAEQAQAFKNEQVLK 360
QY 400 TRVNVILLFMGYMTKDLAIWTCWCESSLYKHLVQETKQFQFOLIDTARQTAQMDYL 459
Db 361 TRVNVILLFMGYMTKQFALITQWCESSLYHHLVADTRFDMVQLIDVARQTAQMDYL 420
QY 460 HAKNIIHRDMKSNFIHLEGLTVKIGDFGLATVKSWSGQQVQPTGSLYVMAPEVIRM 519
Db 421 HAKNIIHRDLKSNFIHLEGLTVKIGDFGLATVKTWSGAQPLEQPSGSLYVMAAEVIRM 480
QY 520 QDNPPESFQSDVTSYGIVLYELMTGELPYSHINNRDQIIPVGRGVASPDLSLYKNCBK 579
Db 481 QDNPPESFQSDVTAIGVLYELMTGSLPYSHIGSDQIIPVGRGVASPDLSLYKNCBK 540
QY 580 AMKRLVADCVKVKKEERPLFPQILSTELQHSPLKPNRSASEPSLHRAHTEINACPL 639
Db 541 AMRRLSDCLKLFQREERPLFPQILATIELLQSLPKIERSASEPSLHR-TQADELPACUL 599
QY 640 TTSPLRP 646
Db 600 SAARLVP 606

RESULT 8

TVFVNM

N: protein kinase (EC 2.7.1.37) mil - avian myelocytomatosis virus MH2
A: Alternate names: kinase-related transforming protein mil (mht); mil proto-oncogene
C: Species: avian myelocytomatosis virus MH2
A: Note: host Gallus gallus (chicken)
C: Date: 27-Nov-1985 #sequence-revision 27-Nov-1985 #text_change 23-Feb-1997

C;Accession: A00639; B00638; A21137
R;Sutrave, P.; Bonner, T.I.; Rapp, U.R.; Jansen, H.W.; Patschinsky, T.; Bister, K.
Nature 309, 85-88, 1984
A;Title: Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine ret
A;Reference number: A00639; MUID:84191511; PMID:6325930
A;Accession: A00639
A;Molecule type: DNA
A;Residues: 1-380 <SUT>
A;Cross-references: GB:K02082
A;Note: The authors translated the codon CAG for residue 58 as Gly
R;Kan, N.C.; Floridellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A;Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by murin
A;Reference number: A00638; MUID:84121298; PMID:6320371
A;Accession: B00638
A;Molecule type: DNA
A;Residues: 1-210,'E',212-380 <KAN>
A;Cross-references: GB:K02084
R;Kan, N.C.; Floridellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 81, 3000-3004, 1984
A;Title: Nucleotide sequence of avian carcinoma virus MH2: two potential onc genes, one
A;Reference number: A21137; MUID:84221892; PMID:6328485
A;Accession: A21137
A;Molecule type: DNA
A;Residues: 1-210,'E',212-230,'E',232-380 <KA2>
A;Cross-references: GB:K02082
C;Comment: This protein is translated as a gag-mht or gag-mil polyprotein.
C;Genetics: mht; mil
A;Gene: mht; mil
C;Superfamily: kinase-related transforming protein; protein kinase homolog
C;Keywords: ATP; oncogene; phosphotransferase; polyprotein; serine/threonine-specific ph
F;80-346/Domain: protein kinase homology <KIN>
F;98-96/Region: protein kinase ATP-binding motif
F;108/Active site: Lys #status predicted

Query Match . 55.3%; Score 1888.5; DB 1; Length 380;
Best Local Similarity 94.7%; Pred. No. 2.5e-91;
Matches 360; Conservative 12; Mismatches 7; Indels 1; Gaps 1;

QY 269 TLPSDSEMTEDAIRSHSESASPSALSSPNNLSPTGWSOPKTPVPAQRERAPVSGTQEN 328
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
2 THPSDSRIIEDAIRNHSESASPSASSSPNNSPTGWSQPPTVPAQRERAPCTNTQEN 61
QY 329 KIIRPGORDSSYYWEIEASEVMLESTRIGSGFGTVYKGWHDVAVKILKVVDPTPEQFO 388
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
62 KIIRPGORDSSYYWEIEASEVLLSTRTIGSGFGTVYKGWHDVAVKILKVVDPTPEQFO 121
QY 389 AFNEVAVLKRTHRVNILLFMGYMTKDNLAIYTWCEGSSLYKHHLHVQETKFQMFLIDI 448
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
122 AFNEVAVLKRTHRVNILLFMGYMTKDNLAIYTWCEGSSLYKHHLHVQETKFQMFLIDI 181
QY 449 ARQTAGMDYLHAKNIIRHDMKSNNIFLHEGLTVTKIGDFGLATVKSRWSGSQQVEQPTGS 508
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
182 ARQTAGMDYLHAKNIIRHDMKSNNIFLHGGLTVKIGDFGLATVKSRWSGSQQVEQPTGS 241
QY 509 VLMWAEVIRMDDNPFQSODVSYGVLYELMTGTLEYSHINNDDQLIIFWVGRYASP 568
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
242 ILMWAEVIRMDDNPFQSODVSYGVLYELMTGTLEYSHINNDDQLIIFWVGRYASP 301
QY 569 DLSKLYKNCPKAMKRLVADCVKKVKREPLFPPOILLSIELLOHSLPKINRSASEPSLHRA 628
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
302 DLSKLYKNCPKAMKRLVADCLKKVREERPLFPPOILLSIELLOHSLPKINRSASEPSLHRA 361
QY 629 AHTEEDINACTLTTSPLPVF 648
DB :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
362 SHTEDINSCTL-TSTRLPVF 380

RESULT 9
TVRHBF
protein kinase B-raf (EC 2.7.1.1-) - human
N;Alternate names: Kinase-related transforming protein B-raf; p94
C;Species: Homo sapiens (man)

C>Date: 31-Dec-1989 #sequence_revision 10-May-1996 #text_change 11-Jun-1999

R/Accession: A57977; A45006; S13798; A31850; I37211
R/Stephens, R.M.; Sathanandam, G.; Copeland, T.; Kaplan, D.R.; Rapp, U.R.; Morrison, unpublished results, 1992, cited by GenBank

A/Description: 95kDa b-Raf serine/threonine kinase: identification of the protein and
A/Reference number: A57977

A/Accession: A57977

A/Molecule type: mRNA

A/Residues: 1-765 <STE>

A/Cross-references: GB:M95712; NID:g179532; PID:AAA35609.1; PID:g179533; GB:M95720;
A/Note: sequence is a composite of those reported in references A45006 and S13798

R/Stephens, R.M.; Sathanandam, G.; Copeland, T.D.; Kaplan, D.R.; Rapp, U.R.; Morrison
Mol. Cell. Biol. 12, 3733-3742, 1992

A/Title: 95-kilodalton B-Raf serine/threonine kinase: identification of the protein a
A/Reference number: A45006; MUID:92375040; PMID:1508179

A/Accession: A45006

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA; protein

A/Residues: 1-115 <ST2>

A/Note: sequence extracted from NCBI backbone (NCBIP:111729)
R:Sathanandam, G.; Kolch, W.; Duh, F.M.; Rapp, U.R.
Oncogene 5, 1775-1780, 1990

A/Title: Complete coding sequence of a human B-raf cDNA and detection of B-raf protei
A/Reference number: S13798; MUID:91133728; PMID:2284096

A/Accession: S13798

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 116-765 <ST>

A/Cross-references: EMBL:X54072; NID:g179532
R/Ikawa, S.; Fukui, M.; Ueyama, Y.; Tamaoki, N.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 8, 2651-2654, 1988

A/Title: B-raf, a new member of the raf family, is activated by DNA rearrangement.
A/Reference number: A31850; MUID:88302178; PMID:3043188

A/Accession: A31850

A/Molecule type: mRNA

A/Residues: 438-765 <IRA>

A/Cross-references: GB:M21001; NID:g179534
R/Eychene, A.; Barnier, J.V.; Apicou, F.; Dutrillaux, B.; Calothy, G.
Oncogene 7, 1657-1660, 1992

A/Title: Chromosomal assignment of two human B-raf(Rml) proto-oncogene loci: B-raf-1
A/Reference number: I37211; MUID:92334878; PMID:1630826

A/Accession: I37211

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-30, 'AGA', 33-199 <EY>

A/Cross-references: EMBL:X65187; NID:g29485; PIDN:CAA46301.1; PID:g29486

C/Genetics:

A/Gene: GDB:BRAF

A/Cross-references: GDB:I27513; OMIM:164757

A/Map position: 7q34-7q34

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
A/Pathway: MAP kinase cascade

A/Note: believed to phosphorylate MAP kinase kinase: found in hippocampal neurons and
C/Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; P
C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-onco
F:234-279/Domain: protein kinase C zinc-binding repeat homology <x22>
F:454-720/Domain: protein kinase homology <XIN>
F:462-470/Region: protein kinase ATP-binding motif
F:234,260,263,279/Binding site: zinc (His, Cys, Cys, Cys)
F:247,250,268,271/Binding site: zinc (Cys, Cys, His, Cys)
F:364,406/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:372/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F:482,500,575,577/Active site: Lys, Glu, Asp, Lys #status predicted
F:728/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 53.5%; Score 1825; DB 1; Length 765;
Best Local Similarity 56.7%; Pred.No 1.le-87;
Matches 379; Conservative 80; Mismatches 167; Indels 42; Gaps 13;

QY 9 KTISNGFGFK-----DAVDFGSSCSIPTIVQQFCYQRRAADGGKLTDPKTSNTIRVF 61
::: ||| | | | | | | | : : : | | | | |

RESULT 9
TVHUBF
protein
N; Altern
C; Specie

Db 100 ESLNGTDFSVSSASMDVTYSSSSSLSVLPSSLSVQNTDVARSNPKSPQKPIVRVF 159
QY 62 LPNKQRTVVNRNGMSLHDCIMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAASL 121
Db 160 LPNKQRTVVPARCGVTVRDSLKALMMRGLIPECCAVYRI--QDGEKKPIGWDTDSLWL 216
QY 122 IGEELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFRQTCGYKFEHCSTKVP 181
Db 217 TGEELHVEVLENVLTTHNFVRKTFFTLAFCDFCRKLFLQGFRCQTCGYKFEHCSTVP 276
QY 182 TMCVDWSNIRQLLFPNPTIGDGVV-----ALPDLMMRRMSVSRRMP--VSSQ 229
Db 277 LMCVNYDQLD--LLFVSFFEHPIPOEASLAETALTSGSPAPASDSIGPOILSPS 334
QY 230 HRYSTPHAFNTWSSPSSEGLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRS--HSE 286
Db 335 PSKSIPIQPFRPADEHNRQFQDRSSAPNVH-INTIEPVN---IDDLIRDQGFGRD 390
QY 287 SASPSALSSSPNNLSPGMSQ----PKTPVPAQERAPVSGTQEKNIIRPGQRDSYYW 342
Db 391 GGSITGLSPASLPGLSTNVKALQKSPGP-QREKSSSSSEDRNRKMTLGRDRSDDW 449
QY 343 EIEASEVMLSTRIGSGSGTGYKKGWHDVAVKILKVVDPPEQFQAFRNEVAVLRKTRH 402
Db 450 EIPDQGITVGRIGSGSGTGYKKGWHDVAVKMLNTVAPTQQLQAFKNEVGLRTRH 509
QY 403 VNILFMGYMKDNLAIYVQWCEGSSLYKHLHVQETKFPQFQFQFQFQFQFQFQFQFQ 462
Db 510 VNILFMGYSTKPLQAIYVQWCEGSSLYKHLHVQETKFPQFQFQFQFQFQFQFQFQFQ 569
QY 463 NLIHRDKSNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVMAPEVIRMQDN 522
Db 570 SLIHRDKSNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVMAPEVIRMQDN 629
QY 523 NPFSQSDVYSGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLYKNCPRAMK 582
Db 630 NPFSQSDVYAFGIVLYELMTGQLPYSINNRDQIIFWVGRGYLSPDLKSVRNCPRAMK 689
QY 583 RLVAQCVKKEERPLFPQILSSLELQHSPLKPNRASEPSLHRAA-HTEDIN--ACTL 639
Db 690 RLMAECLAKKDERPLFPQILASIELLARSUPKIHRSASEPSLNRAGFQTEDFSLYAC-- 747
QY 640 TTSPLRPV 647
Db 748 -ASPKTPI 754

RESULT 10

JN0612
protein kinase B-raf (EC 2.7.1.1), long form - chicken
N:Alternate names: kinase-related transforming protein B-raf; protein kinase Rml1; trans
N:Contains: protein kinase B-raf, short form
C:Species: Gallus gallus (chicken)
C>Date: 24-Feb-1994 #sequence_rev15ion '23-Aug-1996 #text_change 11-Jun-1999
C:Accession: JN0612; S31792
R:Calogeraki, I.; Barnier, J.V.; Eyche, A.; Felder, M.P.; Calothy, G.; Marx, M.
Biochem. Biophys. Res. Commun. 193, 1324-1331, 1993
A:Title: Genomic organization and nucleotide sequence of the coding region of the chicken
A:Reference number: JN0612; MUID:93312327; PMID:832353
A:Accession: JN0612
A:Molecule type: DNA
A:Residues: 1-806 <CAL>
A:Cross-references: EMBL:X67052; NID:963339; PIDN:CAA47436.1; PID:963340
C:Genetics:
A:Gene: c-Rml1
A:Introns: 46/3; 80/3; 168/3; 203/2; 237/3; 287/2; 327/2; 380/2; 393/1; 433/1; 478/3; 511/3
C:Function:
A:Description: member of signal transduction pathway(s) activated by nerve growth factor
A:Pathway: MAP kinase cascade
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; protein
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
nc
F:1-806/Product: protein kinase B-raf, long form #status predicted <MAT>

F:1-392,433-806/Product: protein kinase B-raf, short form #status predicted <SH>
F:235-280/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:495-761/Region: protein kinase ATP-binding motif
F:503-511/Region: protein kinase ATP-binding motif
F:235,261,264,280/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:248,251,269,272/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:365,647/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:373/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F:523/Active site: Lys #status predicted
F:769/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 53.1%; Score 1814; DB 1; Length 806;

Best Local Similarity 52.8%; Pred. No. 4.4e-87;

Matches 382; Conservative 80; Mismatches 149; Indels 112; Gaps 15;

QY 9 KTSNNGFGFR-----DAVFDGSSCISPIVQFGYORASDDGLTDPKSTNIRVF 61

Db 101 ESMGNGTDFSVSSASDTVTASSSSSLSVAPSSSLVYQNTDMMRNNPKSPQKPIVRVF 160

QY 62 LPNKQRTVVNRNGMSLHDCIMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAASL 121

Db 161 LPNKQRTVVPARCGVTVRDSLKALMMRGLIPECCAVYRI--QDGEKKPIGWDTDSLWL 217

QY 122 IGEELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFRQTCGYKFEHCSTKVP 181

Db 218 TGEELHVEVLENVLTTHNFVRKTFFTLAFCDFCRKLFLQGFRCQTCGYKFEHCSTVP 277

QY 182 TMCVDWSNIRQLL-----FPNSTIGDS-GVPALPSLTWR 215

Db 278 LMCVNYDQLDLLFVSFFEHPIQSBETTLGETTPASGYSVPPSSVGGPPLPS---- 333

QY 216 RMRESYRMPVSSQHRISTPHAFNTFTNTSSPSSEGLSQORSTSTPNVHMVSTTLVDSDR 275

Db 334 -----PSPSK---SIPIQPFRPADEHNRQFQDRSSAPNVH-INTIEPVN-- 378

QY 276 MIEDAIRSHS-----ESASPSAL- 293

Db 379 -IDDLIRDQGVREGAPLNQLMRLKRYQSRTSPSLLSVSPSEIVDFEPGVPFRGSTAG 437

QY 294 -----SSSPNNLSPGMSQVQPTVPAQERAPVSGTQEKNIIRPGQRDSYYWEIAS 347

Db 438 LSATPPASLPGLSTNVKALQ-KSPGP-QREKSSSSSEDRNRKMTLGRDRSDDWELPDG 495

QY 348 EVMSTRIGSGSGTGYKKGWHDVAVKILKVVDPPEQFQAFRNEVAVLRKTRHYNILL 407

Db 496 QITVGQIGSGSGTGYKKGWHDVAVKMLNTVAPTQQLQAFKNEVGLRKTRHYNILL 555

QY 408 FMGYMKDNLAIYVQWCEGSSLYKHLHVQETKFPQFQFQFQFQFQFQFQFQFQ 467

Db 556 FMGYSTKPLQAIYVQWCEGSSLYKHLHVQETKFPQFQFQFQFQFQFQFQFQFQ 615

QY 468 DMKSNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVMAPEVIRMQDNPPSP 527

Db 616 DLKSNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVMAPEVIRMQDNPPSP 675

QY 528 QSDVYSGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLYKNCPRAMKRLVAD 587

Db 676 QSDVYAFGIVLYELMTGQLPYSINNRDQIIFWVGRGYLSPDLKSVRNCPRAMKRLMAE 735

QY 588 CVKKVKEERPLFPQILSSLELQHSPLKPNRASEPSLHRAA-HTEDIN--ACTLTSR 644

Db 736 CLAKKDERPLFPQILASIELLARSUPKIHRSASEPSLNRAGFQTEDFSLYAC---ASPK 792

QY 645 LPV 647

Db 793 TPI 795

RESULT 11

I51153

protein kinase B-raf (EC 2.7.1.1), long splice form - quail

N:Alternate names: kinase-related transforming protein B-raf; protein kinase Rml1; tr

N:Contains: protein kinase B-raf, short splice form

C:Species: Coturnix coturnix (quail)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 11-Jun-1999
C:Accession: I51153; I51152
R:Eychene, A.; Barnier, J.
Oncogene 7, 1315-1323, 1992
A:Title: Quail neuroretina c-Rn11(B-raf) protooncogene cDNAs encode two proteins of 93.5
A:Reference number: I51152; MUID:92319540; PMID:1620346
A:Accession: I51153
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-807 <EVC>
A:Cross-references: GB:M80846; NID:g213600; PIDN:AAA49493.1; PID:g213601
A:Accession: I51152
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-392,433-807 <EY2>
A:Cross-references: GB:M80845; NID:g213598; PIDN:AAA49492.1; PID:g213599
C:Genetics:
A:Gene: c-Rn11
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: MAP kinase cascade
A:Note: believed to phosphorylate MAP kinase kinase; found in hippocampal neurons and de
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homologs; prot
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
nc
F:1-392,433-807/Product: protein kinase B-raf, short splice form #status predicted <M2
F:235-280/Domain: protein kinase C zinc-binding repeat homology <K22>
F:495-761/Domain: protein kinase homology <KIN>
F:503-511/Region: protein kinase ATP-binding motif
F:235,261,264,280/Binding site: zinc (His, Cys, Cys, Cys)
F:248,251,269,272/Binding site: zinc (Cys, Cys, His, Cys)
F:365,647/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:373/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
F:523,541,616,618/Active site: Lys, Glu, Asp, Lys #status predicted
F:769/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 53.1%; Score 1814; DB 1; Length 807;
Best Local Similarity 52.8%; Pred. No. 4.5e-87;
Matches 382; Conservative 80; Mismatches 149; Indels 112; Gaps 15;

Qy 9 KTSINGGFGK-----DAVFDGSSCSITVQVQFQRRASDGLDTPSKTSNIRVF 61
Db 101 ESMGNGTDFSVSSASTDTVASSSSLSVAPSSLSVYQNPDMSRNPKSQKPIRVF 160
Qy 62 LPNKQRTVWVRNGMSLHDCIMALKVGRLOPECCAVFRLHHEHKGKARLDWNTDAASL 121
Db 161 LPNKQRTVWPARCGVTVRDSLKKALMRLGLIPECCAVYRI---QDGEKKPIGWDTDISML 217
Qy 122 IGEELQVDFLDHVLTHNFARKTEFLKAFCDICQKFLNGFCQFCGKFEHCSTKYP 181
Db 218 TGEELHVEVLNVPLTHNFVRKTFETFLAFCDICQKFLNGFCQFCGKFEHCSTKYP 277
Qy 182 TMCVDNENIRQLL-----FPNSTIGDS-GVPALPSLWTR 215
Db 278 LMCVNYDQDLDFVSKFEHHPISQETTIGETTPASGYPSPVPSDSVGPPLPS---- 333
Qy 216 RMRESVRMPVSSQHRYSTPHTFTNTSPSSSEGLSQQRQSTSTPNVHMVSTTLPLVDSR 275
Db 334 -----PSPSK---SIPQPFPAEDHRNQFQDRSSAPNVH-INTIEPVN-- 378
Qy 276 MIEDAIRSHS-----ESASPSAL----- 293
Db 379 -IDDLIRDOQVRGEGAPLNLMRLRKYSQRTSPSLHLSVPSIVDFEFGPVFRGSTAG 437
Qy 294 -----SSSPNNLSPTGWSQPKTPVPAQRARAVSGTQENKLRPRGQDRSSYIWEIAS 347
Db 438 LSATPPASLPGSLTNVAKLQ-KSPGP-QREKSSSSSEDENRKMTLGRDSSDDWEIPDG 495
Qy 348 EVMLESTRIGSGSGTGVYKKGWGDVAVKILKVVDPTEPQAPRNEAVLRKTRHVNILL 407
Db 496 QITVGRIGSGSGTGVYKKGWGDVAVKILKVVDPTEPQAPRNEAVLRKTRHVNILL 555

Qy 408 FMGWTQNTLAIVTQWCBSGLYKHLHVQETKFFOMFOLIDIARTAGQMDYLHAKNIHR 467
Db 556 FMGISTKPLQLAIVTQWCBSGLYHHLHIIETKFFEMIKLIDIARTAGQMDYLHAKSIHR 615
Qy 468 DMKSNNIFLHGLTVKIGDFGLATVKSWSGSOQVEOPTGSGVLWMAPEVIRMDNNPESF 527
Db 616 DLKSNNIFLHGLTVKIGDFGLATVKSWSGSHGFQELSGSILWMAPEVIRMDQKNPISF 675
Qy 528 QSDVYSGIVLYELMTGELPYSHINNRRDQIIFMVGSGYASPDLSKLYKNCPKAMKRLVAD 587
Db 676 QSDVYAFGIVLYELMTGOLPYSNINNRRDQIIFMVGSGYASPDLSKLYKNCPKAMKRLMAE 735
Qy 588 CVKKVKEPRLFPQILSIQLLQHSLSKPKNSASEPSLHRAA-HTEIDN--ACTLTTSR 644
Db 736 CLKKKRDERPLFPQILASIELLARSLSPKIHSASEPSLNRAGFTQEDFSLYAC---ASPK 792
Qy 645 LPV 647
Db 793 TPI 795

RESULT 12
TMVVF6
protein kinase (EC 2.7.1.37) raf - murine sarcoma virus 3611
N:Alternate names: kinase-related transforming protein raf; raf. proto-oncogene protel
C:Species: murine sarcoma virus 3611
A:Note: host Mus musculus (mouse)
C:Accession: A00638; #sequence_revision 27-Nov-1985 #text_change 23-Feb-1997
R:Kan, N.C.; Flordellia, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A:Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by mu
A:Reference number: A00638; MUID:84121298; PMID:6320371
A:Accession: A00638
A:Molecule type: DNA
A:Residues: 1-323 <KAN>
A:Experimental source: ATCC 45010
R:Mark, G.E.; Rapp, U.R.
Science 224, 285-289, 1984
A:Title: Primary structure of v-raf: relatedness to the src family of oncogenes.
A:Reference number: A38020; MUID:84172180; PMID:6324342
A:Accession: A38020
A:Molecule type: DNA
A:Residues: 1-323 <MAR>
C:Comment: This protein is translated as a gag-raf polyprotein.
C:Genetics:
A:Gene: raf
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kina
F:22-288/Domain: protein kinase homology <KIN>
F:30-38/Region: protein kinase ATP-binding motif
F:50/Active site: Lys #status predicted

Query Match 48.5%; Score 1654; DB 1; Length 323;
Best Local Similarity 97.2%; Pred. No. 3.2e-79;
Matches 314; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 326 EKNKTRPRGQDRSSYIWEIASVLMSTRIGSGFGTVYKKGWGDVAVKILKVVDPTEP 385
Db 1 EKNKTRPRGQDRSSYIWEIASVLMSTRIGSGFGTVYKKGWGDVAVKILKVVDPTEP 60
Qy 386 QFOAERNEAVLRKTRHVNILLFMGYMTKDNLAIVTQWCBSGLYKHLHVQETKFOFQL 445
Db 61 QLOAERNEAVLRKTRHVNILLFMGYMTKDNLAIVTQWCBSGLYKHLHVQETKFOFQL 120
Qy 446 IDIARTAGQMDYLHAKNIHRDKSNNIFLHGLTVKIGDFGLATVKSWSGSOQVEQP 505
Db 121 IDIARTAGQMDYLHAKNIHRDKSNNIFLHGLTVKIGDFGLATVKSWSGSOQVEQP 180
Qy 506 TGSVLWMAPEVIRMDNNPFSQSDVYSGIVLYELMTGELPYSHINNRRDQIIFMVG 565
Db 181 TGSVLWMAPEVIRMDNNPFSQSDVYSGIVLYELMTGELPYSHINNRRDQIIFMVG 240

QY	566	ASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINSASEPSL	625
Db	241	ASPDLSRLYKNCPKAIKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINSASEPSL	300
QY	626	HRAAHTEDINACTLTSPRLPVF	648
Db	301	HRAAHTEDINACTLTSPRLPVF	323
RESULT 13			
TVMSRF			
protein kinase A-raf-1 (EC 2.7.1.-) - mouse (fragment)			
N:Alternate names: A-raf-1 proto-oncogene protein-serine/threonine kinase; kinase-related			
C:Species: Mus musculus (house mouse)			
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999			
C:Accession: A25382			
R:Huleihel, M.; Goldsborough, M.; Cleveland, J.; Gunnell, M.; Bonner, T.; Rapp, U.R.			
Mol. Cell. Biol. 6, 2655-2662, 1986			
A:Title: Characterization of murine A-raf, a new oncogene related to the v-raf oncogene.			
A:Reference number: A25382; MUID:87064566; PMID:3491291			
A:Accession: A25382			
A:Molecule type: mRNA			
A:Residues: 1-437 <HUL>			
A:Cross-references: GB:M13071; NID:g192016; PIDN:AAA37258.1; PID:g387104			
C:Genetics:			
A:Gene: A-raf			
C:Function:			
A:Description: signal transduction between cell membrane and nucleus; after phosphorylat			
A:Pathway: MAP kinase cascade			
A:Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tissues			
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot			
C:Keywords: Atp; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene			
F:139-405/Domain: protein kinase homology <KIN>			
F:147-155/Region: protein kinase ATP-binding motif			
F:147/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted			
F:56/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted			
F:167/Active site: Lys #status predicted			
F:413/Binding site: phosphate (Ser) (covalent) #status predicted			
Query Match 41.3%; Score 1409.5; DB 1; Length 437;			
Best Local Similarity 66.7%; Pred. No. 2.3e-66;			
Matches 275; Conservative 53; Mismatches 71; Indels 13; Gaps 6;			
QY	243	SSPSEGLSQSORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSEA-----SPSALSS	295
Db	31	SFPAPANPPLQIRISTSTPNVHMVSTTAPMDSSLMQFTAQSFSTDAAGRGDAPRG-SP	89
QY	296	SPNNLSPTGWSQKTPVPA-QREAPVSGTQEKNKIRPGORDSSYWEIEASEVWLSTR	354
Db	90	SPASVS-SGRKSPHSKLPSEQRERKSLA--DEKKYKNLGYRDSGYWEVPPSEVQLKR	146
QY	355	IGSGSFGTVYKKGWGDVAVKILKVDPTPEQFQAFRNEVAVLKRTRHVNILLFMGYTK	414
Db	147	IGTSGTVYFGLHGDVAVKVLKVAQPTAEQAQAKFQEMQVLRKTRHVNILLFMGFMR	206
QY	415	DNLAIVTQWCSESSLYKHLHVQETKFOFOLIDIARTQAGMDYLHAKNIIHDMKSNNI	474
Db	207	PGFALITQWCSESSLYKHLHVADTFDMVQLIDVARTQAGMDYLHAKNIIHRLKSNNI	266
QY	475	FLHGLTVIKIGDFGLATVKSNSGSGQVEQPTGSLVMAPEVIRMODNPNPESQSDVSY	534
Db	267	FLHGLTVIKIGDFGLATVKTWSGAQPLEQPSGSLVMAAEVIRMQDPNPYFSQSDVIAY	326
QY	535	GIVLYELMTGELPYSHNNRQIIFVMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKE	594
Db	327	GVVLYELMTGSLPYSHIGSRDQIIFVMVGRGLYSPDLSKIFSNCPKAMRLLTDCLKQRE	386
QY	595	ERPLFPQILSSIELLQHSPLKINSASEPSLHRAAHTEDINACTLTSPRLP	646
Db	387	ERPLFPQILATLQRLSLPKIERSASEPSLHR-TQADLPACLLSAAALVP	437
RESULT 14			
S47244			
C:raf protein - zebra fish			
C:Species: brachydanio rerio (zebra fish)			
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999			
C:Accession: S47244			
R:Daniotti, J.L.			
submitted to the EMBL Data Library, August 1994			
A:Reference number: S47244			
A:Accession: S47244			
A>Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-307 <DAN>			
A:Cross-references: EMBL:X81128; NID:g534976; PIDN:CAA57035.1; PID:g534977			
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom			
C:Keywords: Atp			
F:7-273/Domain: protein kinase homology <KIN>			
F:15-23/Region: protein kinase ATP-binding motif			
Query Match 41.0%; Score 1398.5; DB 2; Length 307;			
Best Local Similarity 88.1%; Pred. No. 5.8e-66;			
Matches 266; Conservative 20; Mismatches 15; Indels 1; Gaps 1;			
QY	347	SEVMLSTRIGSGSGFTGVYKKGWGDVAVKILKVDPTPEQFQAFRNEVAVLKRTRHVNIL	406
Db	7	NEVLLSRIGSGSGFTGVYKKGWGDVAVKLVKVTNPTPEQFQAFRNEVAVLKRTRHVNIL	66
QY	407	LFGYMTKDNLAIVTQWCSESSLYKHLHVQETKFOFOLIDIARTQAGMDYLHAKNIIH	466
Db	67	LFGYMTKGNLAIVTQWCSESSLYKHLHVLETFQFOLIDIARTQAGMDYLKMKHIH	126
QY	467	RDMSNNIFLHGLTVIKIGDFGLATVKSNSGSGQVEQPTGSLVMAPEVIRMODNPNFS	526
Db	127	RDMSNNIFLHGLTVIKIGDFGLATVTKARNSGSGQVEQPSGSLVMAPEVIRMQDNNPYS	186
QY	527	FQSDVYSYGLVYELMTGELPYSHNNRQIIFVMVGRGYASPDLSKLYKNCPCAMKRLVA	586
Db	187	FQSDVYSYGLVYELMTGELPYSQIGNRQIIFVMVGRGLYSPDLSKLYKRCPCAMKRLVA	246
QY	587	DCVKVKEERPLFPQILSSIELLQHSPLKINSASEPSLHRAAHTEDINACTLTSPRLP	646
Db	247	DCIKSKDERPLFPQILSSIELLQHSPLKINSASEPSLHRSASQSEDISSCTL-TSMKLP	305
QY	647	VF 648	
Db	306	VF 307	
RESULT 15			
TVFDF			
protein kinase Draf-1 (EC 2.7.1.-) - fruit fly (Drosophila melanogaster)			
N:Alternate names: Draf-1 proto-oncogene protein-serine/threonine kinase; kinase-rela			
C:Species: Drosophila melanogaster			
C>Date: 31-Mar-1991 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1997			
C:Accession: S00393; S60191; A27808; S33602			
R:Nishida, Y.; Hata, M.; Ayaki, T.; Ryo, H.; Yamagata, M.; Shimizu, K.; Nishizuka, Y.			
EMBO J. 7, 775-781, 1988			
A:Title: Proliferation of both somatic and germ cells is affected in the Drosophila m			
A:Reference number: S00393; MUID:88283647; PMID:3135183			
A:Accession: S00393			
A:Molecule type: DNA			
A:Residues: 1-781 <NIS>			
A:Cross-references: EMBL:X07181			
A:Note: the assignment of the start codon has been revised in reference S33602			
A:Accession: S60191			
A:Molecule type: mRNA			
A:Residues: 148-781 <NIS2>			
R:Mark, G.E.; MacIntyre, R.J.; Digan, M.E.; Ambrosio, L.; Perrimon, N.			
Mol. Cell. Biol. 7, 2134-2140, 1987			
A:Title: Drosophila melanogaster homologs of the raf oncogene.			
A:Reference number: A27808; MUID:87257926; PMID:3037346			
A:Accession: A27808			
A:Molecule type: mRNA			
A:Residues: 'LQ', 465-519, 'R', 521, 'A', 523-570, 'R', 572-699, 'PQAL', 704-713, 'PT', 716-753			

R; Sprenger, F.; Troscclair, M.M.; Morrison, D.K.
Mol. Cell. Biol. 13, 1163-1172, 1993
A: Title: Biochemical analysis of torso and D-raf during Drosophila embryogenesis: implication of the protein kinase C zeta-binding repeat homology <K22>
A: Reference number: S33602; MUID: 93140754; PMID: 8423783
A: Contents: annotation
A: Note: this is a revision of the assignment of the start codon in reference S00393
A: Note: the authors call the N-terminal extended version of the protein Draf-3
A: Note: the cited sequence in S33602 shows Pro for residue 342
C: Genetics:
A: Gene: Draf-1
A: Cross-references: FlyBase: FBgn0003079
A: Map position: X 2F
A: Introns: 417/3; 464/3; 589/2
C: Superfamily: protein kinase A-raf; protein kinase C zeta-binding repeat homology; protein kinase C zeta-binding repeat homology; serine/threonine-specific protein kinase
F: 265-310/Domain: protein kinase C zeta-binding repeat homology <K22>
F: 469-735/Domain: protein kinase C zeta-binding repeat homology <KIN>
F: 477-485/Region: protein kinase ATP-binding motif
F: 497/Active site: Lys #status predicted

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Query Match          40.0%; Score 1365; DB 1; Length 781;
Best Local Similarity 46.4%; Pred. NO. 9.2e-64;
Matches 304; Conservative 86; Mismatches 193; Indels 72; Gaps 16;

QY 32 IVQFGYQRRASDDGKLT-----PSKTSNT-----INVFLPNKQRTVVVNRNMSL 78
DQ 146 ILQQRQLARVHHGTDLDSLGSPGSGCGTLTRQPKILLRAHLPNQORTSVEVISGRL 205
QY 79 HDCLMKALKVGLQPECAVRLLEHKKARLDWNTDAASLIGELQVDFLDHVLPTT 138
DQ 206 CDALMKALKQLPTDMCEVST---THSGRHI-IPWHTDITGLHVEIFVRLLDKFPRT 261
QY 139 ---HNFARKTEFLKAFCDICQKELLNGFRCTCYKKEHCSTKVPVPCVDM--SNIRQL 193
DQ 262 HIKHQLINKTFEFLVFCGECRRLLFTGYCSQCNEFRHQRANRVPMLCQPPMDSYQL 321
QY 194 LIFNSTIGSGVPALPSLTMRMRSESVSRMPVSSQHRYSYTHAFNTSS--PSSEGS- 250
DQ 322 LLAENP---DNGV-GFPG-----RGTAVRFNKSSRSRRSSSGSSSSSKPPSSSGN 371
QY 251 -----LSQRORSTSPNV---HMVSTLPLVDSDMIEDA-----IRSHSESASPSA 292
DQ 372 HRQRPPIRISQDDKSNAPNCININRSVTSEVQSLIMOARPLPHPCPTDHSNSTQASP 431
QY 293 LSSSPNNLPTGWSQKPTVPVPAQRERAPVSGTQKKNKIRPRGORDSSYYWEIEASEVMLS 352
DQ 432 TSTLKH-----RPRARSADESNKLL--RDAKSEENWNILAEILIG 474
QY 353 TRIGSGSGFYVYKKGHGVAVKILKVVDTPPEQFAFRNEVAVLRKTRHVNILLFMGYM 412
DQ 475 PRIGSGSGFYVYRAHVGVPVAVKTLNVKTPSPAQLQAFKNEVAMLKTRHCNILLFMGCV 534
QY 413 TKDNLAIQTQWCGSSLYKHLHVQETKFMQFQIDTARQAGMDYLHAKNIHHRDKSN 472
DQ 535 SKPSLAIVTQWCGSSLYKHLHVQETKFMQFQIDTARQAGMDYLHAKNIHHRDKSN 594
QY 473 NIFLHGLVTKIGDFGLATVKSWSGSQQVEPTGSVLWMAPEVIRMQDNNPFQSDVY 532
DQ 595 NIFLHGLVTKIGDFGLATVKSWSGSQQVEPTGSVLWMAPEVIRMQDNNPFQSDVY 654
QY 533 SYGIVLYELMTGLPYSHINRDQIIFMYGRGYPSPDLKLYKNCPKAMKRLVADCVKRY 592
DQ 655 AFGIVMYELLAECPLPGHISNKKDQILFMVGRLLPDMDSQVRSDDARRHKKRAEDCIKYT 714
QY 593 KEERPLFPQILSLIHLQSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPV 647
DQ 715 PKDRPLRPLNMLNMLTLPLKIHRSASEPNLTQSQDND--EFLYLPSPKTPV 767
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Search completed: July 9, 2003, 09:46:42
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:46:18 ; Search time 28 Seconds
(without alignments)
2694.286 Million cell updates/sec

Title: US-09-637-302c-2
Perfect score: 3413
Sequence: 1 MEHIQGAWKTSINGFGFKDA.....AHTEDINACTITTSPLPVF 648

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB_PEP.*
5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB_PEP.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB_PEP.*
7: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB_PEP.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB_PEP.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB_PEP.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3413	100.0	648	9 US-09-513-145-6	Sequence 6, Appl
2	3413	100.0	648	9 US-10-059-585-38	Sequence 38, Appl
3	1891.5	55.4	604	9 US-10-205-342-1	Sequence 1, Appl
4	1165	34.1	271	10 US-09-840-704-6	Sequence 6, Appl
5	1143	33.5	217	9 US-09-513-145-5	Sequence 5, Appl
6	786	23.0	148	9 US-09-513-145-4	Sequence 4, Appl
7	646	18.9	125	10 US-09-925-302-849	Sequence 849, App
8	457.5	13.4	850	10 US-09-904-389-2	Sequence 2, Appl
9	422.5	12.4	263	10 US-09-840-704-5	Sequence 5, Appl
10	404	11.8	505	9 US-09-977-260-6	Sequence 6, Appl
11	404	11.8	505	9 US-09-977-261-6	Sequence 6, Appl
12	404	11.8	505	10 US-09-977-269-6	Sequence 6, Appl
13	404	11.8	505	10 US-09-982-610-20	Sequence 20, Appl
14	403	11.8	537	9 US-09-977-260-11	Sequence 11, Appl
15	403	11.8	537	9 US-09-977-261-11	Sequence 11, Appl
16	403	11.8	537	10 US-09-977-269-11	Sequence 11, Appl
17	400	11.7	537	10 US-09-771-161A-212	Sequence 212, App
18	400	11.7	537	10 US-09-771-161A-213	Sequence 213, App
19	397	11.6	536	9 US-09-977-260-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-513-145-6
; Sequence 6, Application US/09513145
; Publication No. US20020192723A1
; GENERAL INFORMATION:
; APPLICANT: Yoo, Rai-June
; TITLE OF INVENTION: Antigen to Systemic Lupus Erythematositis and Diagnostic
; FILE OF INVENTION: Assay
; FILE REFERENCE: 2502-1-2
; CURRENT APPLICATION NUMBER: US/09/513,145
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121548
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-145-6

Query Match 100.0%; Score 3413; DB 9; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.6e-246;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEHIQGAWKTSINGFGFKDAVFDGSSCISPTIVQFGYQRRASDDGKLTDPKSTNIRV	60
DB	1	MEHIQGAWKTSINGFGFKDAVFDGSSCISPTIVQFGYQRRASDDGKLTDPKSTNIRV	60
QY	61	FLPNKQRTVVVNRNGSHLDCMLKALKVRGLQPECCAVFLLHEHKGKARLDWNTDAAS	120
DB	61	FLPNKQRTVVVNRNGSHLDCMLKALKVRGLQPECCAVFLLHEHKGKARLDWNTDAAS	120
QY	121	LIGEEQVDFLDHVPVLTTHNFARKTFLKLAFCDCICOKFLLNGFRCTCGYKHEHCSTKV	180
DB	121	LIGEEQVDFLDHVPVLTTHNFARKTFLKLAFCDCICOKFLLNGFRCTCGYKHEHCSTKV	180
QY	181	PTMCVDWSNIRQLLLFPNSTIGDSGVPAFPALPSLTMRMRRESVSRMPYSSQHRYSTPHATF	240
DB	181	PTMCVDWSNIRQLLLFPNSTIGDSGVPAFPALPSLTMRMRRESVSRMPYSSQHRYSTPHATF	240
QY	241	NTSSPSSEGLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESAPSSALSSPNNL	300

Db 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLPLVDNRMIEDAIRSHSESASPALSPPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSGTQENKIRPRRGORDSSYYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQENKIRPRRGORDSSYYWEIEASEVYMLSTRIGSGSF 360
Qy 361 GTVYKGKWHGDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILLFNGYMTKDNLAIV 420
Db 361 GTVYKGKWHGDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILLFNGYMTKDNLAIV 420
Qy 421 TQWCEGSSLYKHLHVQETKFOFQOLIDIARQTAQGMVYLAHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFOFQOLIDIARQTAQGMVYLAHAKNIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRWSSGQOQVPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWSSGQOQVPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 2

US-10-059-585-38
; Sequence 38, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 3413; DB 9; Length 648;
US-10-059-585-38

Best Local Similarity 100.0%; Pred. No. 2.6e-246;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEHIQGAWKTTISNGFGFKDAVDFDGGSSCISPTIVQFGVQRRASDDGKLTDPSTKTSNTIRV 60
Db 1 MEHIQGAWKTTISNGFGFKDAVDFDGGSSCISPTIVQFGVQRRASDDGKLTDPSTKTSNTIRV 60
Qy 61 FLPNKQRTVVNVNRGMSLHDCIMKALKVIRGLQPECCACVAFRLHHEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVNRGMSLHDCIMKALKVIRGLQPECCACVAFRLHHEHKGKARLDWNTDAAS 120
Qy 121 LIGBELQVDFLDHVPVLTTHNFARKTFLKAPCDICQKFLNGLPRCQCCTGKFKFHEHCSTKV 180
Db 121 LIGBELQVDFLDHVPVLTTHNFARKTFLKAPCDICQKFLNGLPRCQCCTGKFKFHEHCSTKV 180
Qy 181 PTMCDVNSINIRQLLLFPNSTIGDSVPALPSLTMRNRRESVSRMPVSSQHRISTPHAFTF 240
Db 181 PTMCDVNSINIRQLLLFPNSTIGDSVPALPSLTMRNRRESVSRMPVSSQHRISTPHAFTF 240
Qy 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLPLVDNRMIEDAIRSHSESASPALSPPNNL 300
Db 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLPLVDNRMIEDAIRSHSESASPALSPPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSGTQENKIRPRRGORDSSYYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQENKIRPRRGORDSSYYWEIEASEVYMLSTRIGSGSF 360
Qy 361 GTVYKGKWHGDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILLFNGYMTKDNLAIV 420
Db 361 GTVYKGKWHGDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILLFNGYMTKDNLAIV 420
Qy 421 TQWCEGSSLYKHLHVQETKFOFQOLIDIARQTAQGMVYLAHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFOFQOLIDIARQTAQGMVYLAHAKNIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRWSSGQOQVPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWSSGQOQVPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 3

US-10-205-342-1
; Sequence 1, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnoch, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: A-raf protein (AA 1-604)
US-10-205-342-1

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Query Match      55.4%; Score 1891.5; DB 9; Length 604;
Best Local Similarity 61.7%; Pred. No. 7.2e-133;
Matches 377; Conservative 76; Mismatches 125; Indels 33; Gaps 10;

QY 50 DPKSTNTIRVLPNKHQRTVVVVRNGSLHDLCKALKKVRGLQPECCAVFLLHEHGKK 109
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
13 EPSRAVGVKRVLPNKHQRTVVVVRNGSMVYDLSLDKALKVRGLNQDCCVYRLI---KGRK 69

QY 110 ARLDWNTDAASLIGEEQLQVDFLDHVPLTTNHFARKTEFLKLAFCDCOKETLLGFRCTCG 169
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
70 TVTAWDAIAPLDGEELIVELEVDPLTMHNFYKTFEFLAFCDFLKFHGFRCOTCG 129

QY 170 YKFEHSTKVPKVCVWMS-NIROLFLPNSTIGSGVPALPSLTMRMRESVSRMPVSS 228
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
130 YKPHOCSKVPKVCVWMSNRQFYHSIQDLSSGGS-----RQCEVPSNLSVNE 178

QY 229 QHRYSTPHAF-----FNTSSPSSGSLSORQSTSTPNVHMVSTLTPVDSRMIEDAIRS 283
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
179 LLTPQGPSPTQQRDQEHFEPAPANPLQRIKSTSTPNVHMVSTTAPMDSLSMQFTAQS 238

QY 284 HSEA-----SPSALSSSPNNLSPTGWSQPKTPVPA-QRERAPVSGTGKKNKIRPRGQ 335
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
239 FSTDAAGRGGDGAPRG-SPSPASVS-SGRKSPHSKLPAEQRERKSLA--DEKKVKNLGY 294

QY 336 RDSYYWEIEASEVMLSTRIGSGSGFYVYKKGWGDVAVKILKVVDPTPQFOAFRNEVA 395
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
295 RDSYYWEVPPSEVQLKRIKRGTSFGTVFRGRHGDVAVKLVKVAQPTAEQAQAFKNEQ 354

QY 396 VLKTRHVNILLFGYMTKDNLAIVTQWCEGSSLYKHLHVOETKFMQLIDTAROTAG 455
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
355 VLKTRHVNILLFGWFTRGFAITQWCEGSSLYHHLHVDVRFVQVQIDVAROTAG 414

QY 456 MDYLHAKNIHRLMKSNNIFLHGLTVKIGDFGLATVKSRWSGQVQPTGSLVMAPE 515
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
415 MDYLHAKNIHRLMKSNNIFLHGLTVKIGDFGLATVKSRWSGQVQPTGSGVLMWAAE 474

QY 516 VIRMQDNPFSFSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLY 575
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
475 VIRMQDNPFSFSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLY 534

QY 576 NCPKAMKRLVADVCKVKEPPLFPQILSSIELLQHSPLKRNASSEPSLHRAAHTEDIN 635
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
535 NCPKAMRLLTDLKFORERPLFPQILATIELQHSPLKRIEASSEPSLHR-TQADELP 593

QY 636 ACTLTSPLRP 646
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
594 ACLLSAARLVP 604
```

```
RESULT 4
US-09-840-704-6
; Sequence 6, Application US/09840704
; Patent No. US20020122801A1
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
; FILE REFERENCE: KIN-2CON
; CURRENT APPLICATION NUMBER: US/09/840,704
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/566,906
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US08/752,345
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 271
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
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; LOCATION: (1)....(271)
US-09-840-704-6

Query Match      34.1%; Score 1165; DB 10; Length 271;
Best Local Similarity 80.4%; Pred. No. 3.8e-79;
Matches 218; Conservative 25; Mismatches 28; Indels 0; Gaps 0;

QY 344 IEASEVMLSTRIGSGSGFYVYKKGWGDVAVKILKVVDPTPQFOAFRNEVAVLRKTRHV 403
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 IPDQITVQORIGSGSGFYVYKKGWGDVAVKMLNVTAPTQQLQAFKNEVGLVRKTRHV 60

QY 404 NILFMGYMTKDNLAIVTQWCEGSSLYKHLHVOETKFMQLIDTAROTAGMDYLHAKN 463
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 NILFMGYSTKQLAIVTQWCEGSSLYHHLHIEKFEKIKLIDTAROTAGMDYLHAKS 120

QY 464 IHRDMKSNNIFLHGLTVKIGDFGLATVKSRWSGQVQPTGSLVMAPEVIRMQDNN 523
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
121 IHRDLKSNIFLHEDLTVKIGDFGLATVKSRWSGSHQEQLSGSLMMAPEVIRMQDKN 180

QY 524 PFSFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLYKNCPKAMKR 583
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
181 PFSFQSDVYAFGLVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLYKNCPKAMKR 240

QY 584 LVADCVKVKYKEPPLFPQILSSIELLQHSPL 614
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
241 LMAECLKKRDERPLFPQILASIELLARSPL 271
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```
RESULT 5
US-09-513-145-5
; Sequence 5, Application US/09513145
; Publication No. US20020192723A1
; GENERAL INFORMATION:
; APPLICANT: Yoo, Tai-June
; TITLE OF INVENTION: Antigen to Systemic Lupus Erythematosus and Diagnostic
; FILE REFERENCE: 2502-1-2
; CURRENT APPLICATION NUMBER: US/09/513,145
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121548
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-145-5

Query Match      33.5%; Score 1143; DB 9; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.2e-77;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 GFCOTCGYKFEHCSTKVPKVCVWMSNIROLFLPNSTIGSGVPALPSLTMRMRESV 221
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 GFCOTCGYKFEHCSTKVPKVCVWMSNIROLFLPNSTIGSGVPALPSLTMRMRESV 60

QY 222 SRMPVSSQHRYSTPHAFTEFTNTSSPSSGSLSORQSTSTPNVHMVSTLTPVDSRMIEDAI 281
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 SRMPVSSQHRYSTPHAFTEFTNTSSPSSGSLSORQSTSTPNVHMVSTLTPVDSRMIEDAI 120

QY 282 RSHSESASPSALSSPNLSPTGWSQPKTPVPAQRERAPVSGTGKKNKIRPRGQDSSYY 341
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
121 RSHSESASPSALSSPNLSPTGWSQPKTPVPAQRERAPVSGTGKKNKIRPRGQDSSYY 180

QY 342 WEIEASEVMLSTRIGSGSGFYVYKKGWGDVAVKILK 378
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
181 WEIEASEVMLSTRIGSGSGFYVYKKGWGDVAVKILK 217
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RESULT 6
US-09-513-145-4
; Sequence 4, Application US/09513145
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Publication No. US20020192723A1
GENERAL INFORMATION:
APPLICANT: Yoo, Tai-June
TITLE OF INVENTION: Antigen to Systemic Lupus Erythematosus and Diagnostic
FILE REFERENCE: 2502-1-2
CURRENT APPLICATION NUMBER: US/09/513,145
CURRENT FILING DATE: 2000-02-25
EARLIER APPLICATION NUMBER: 60/121548
EARLIER FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 148
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-145-4

Query Match      23.0%; Score 786; DB 9; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.1e-51;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHQGAWKTSINGFGKDAVFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHQGAWKTSINGFGKDAVFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLPNKQRTVVNRGMSLHDLCKALKVRLGLOPECCAVFLLHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNRGMSLHDLCKALKVRLGLOPECCAVFLLHEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPLTHNFARKTFLK 148
DB 121 LIGELQVDFLDHVPLTHNFARKTFLK 148

RESULT 7
US-09-925-302-849
Sequence 849, Application US/09925302
Patent No. US2002004941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAL04
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 849
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (113)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (116)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (118)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-849

Query Match      18.9%; Score 646; DB 10; Length 125;
Best Local Similarity 96.8%; Pred. No. 6.9e-41;
Matches 120; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Publication No. US2002012940A1
GENERAL INFORMATION:
APPLICANT: Clendennen, Stephanie K.
APPLICANT: Schuster, Debra K.
TITLE OF INVENTION: CTRL HOMOLOGUE FROM MELON
FILE REFERENCE: 4257-0029.30
CURRENT APPLICATION NUMBER: US/09/904,389
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/218,307
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 850
TYPE: PRT
ORGANISM: Cucumis melo
FEATURE:
NAME/KEY: VARIANT
LOCATION: (154)...(154)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-904-389-2

Query Match      13.4%; Score 457.5; DB 10; Length 850;
Best Local Similarity 35.3%; Pred. No. 1e-25;
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;

QY 288 ASPSALSSSP-----NNLSPTGWSQPKTPVPAQRERAP-----VSGTQ--EKNKI 330
DB 503 ASFYVQSTPFVENVVPLSHISHISESEHLLALSHRMDHVNLLPFVHGSOLIRKNE 562
QY 331 RPRGQRDSSYYWEIEASEVYMLSTRIGSGFGVYVKGKWHG-DVAVKILKVVDPDPEQFOA 389
DB 563 LSLGLEDLVIPW----TDLDLREKIGAGSGFGVYVKGWHSVDVAVKILTEQDFHPYRNE 618
QY 390 FRNEAVLRKTRHVNLLEFNGYTK-DNLAIYTONCEGSSLYKHLH-----VQETKQOM 442
DB 619 FLREVAIMKSLRHPNIVLFMGAVTTPPNLSIVTELSRGSLLRLLHKGSKVDIDETR--- 675
QY 443 FOLIDILAROTACMDYLHAKN--IHRDMKSNIFLHEGLTVKIGDFGLATVKSWSGQ 500
DB 676 --RINAFDVAKGMVYLRHDPPIVHRDLKSPNLLVDKKTIVKVCDFGLSRKARTFLSS 733
QY 501 QVEQPTGSLVMAPEVIRMODNNPFSQSDVTSYGIYLYELMTGELPYSHINNRQIIFM 560
DB 734 --KSAAGTPEWNAPEVLR---DEPSNEKSDVTSYSGVILWELATLQOPMCNLPN-QVVA 787
QY 561 VGRGYASPDLSKLYKNCPRKMLRVADCVKVKKEERPLFPQILSLSTELLQSLP 614
DB 788 VGFKGKRLDIPRVN--PKLASLIVA-CWADEPWKRPFSSIMETLKPKTKQAP 838

RESULT 9
US-09-840-704-5
Sequence 5, Application US/09840704
Patent No. US20020122801A1
GENERAL INFORMATION:
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Search completed: July 9, 2003, 09:52:20
Job time : 30 secs

US-09-977-260-11

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Query Match      11.8%; Score 403; DB 9; Length 537;
Best Local Similarity 35.7%; Pred. No. 6.3e-22;
Matches 97; Conservative 55; Mismatches 100; Indels 20; Gaps 9;

QY 342 WEIEASEVMLSTRIGSGFGTVYKWKHGD--VAVKILKVVDPTPEQFOAFRNEVAVLRK 399
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 264 WEIPRESLQIKRLNGQGFGEWMGTWNGTKVAIKTLKPGTMSPE---SFLAEAQIMKK 320
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 400 TRHVNILLFMGTWTKDNLAIVTQWCEGSSLYKHLHVQETK-FQMFQLIDIAROTAQGM DY 458
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 321 LKHDKLVLQLYAVVSEPIYIVTEYMNKGSLLDFLDKGEGRAIKLPNLVDMAAQVAAGMAY 380
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 459 LHAKNIIHRDMKSNIFLHEGLTVKIGDFGLATV--KSRWSGQQVEQPTGSLVWMAPEV 516
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 381 IERNMYIHRDLRSANILVGNGLICKIADFGLARLIEDNEYTARQAKFP---IKWTAPEA 437
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 517 IRMQDNNPFSQSDYISYGIYLYELMT-GELPYSHINNRDQIIFMVGRGYASPDLSKLYK 575
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 438 ALY---GRTFKSDVNSFGILLTELVTGKRVPGCMNNR-EVLEQVERGYRMP-----CPQ 489
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 576 NCPKAMKRLVADCVKVKKEERPLFPQILSSIE 607
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 490 DCPISLHELMHCKKDPPEPTFEYLSQSFLE 521
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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RESULT 15

```
US-09-977-261-11
; Sequence 11, Application US/09977361
; Publication No. US20030054527A1
; GENERAL INFORMATION:
; APPLICANT: ULRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-261-11
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```
Query Match      11.8%; Score 403; DB 9; Length 537;
Best Local Similarity 35.7%; Pred. No. 6.3e-22;
Matches 97; Conservative 55; Mismatches 100; Indels 20; Gaps 9;

QY 342 WEIEASEVMLSTRIGSGFGTVYKWKHGD--VAVKILKVVDPTPEQFOAFRNEVAVLRK 399
    ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 264 WEIPRESLQIKRLNGQGFGEWMGTWNGTKVAIKTLKPGTMSPE---SFLAEAQIMKK 320
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 400 TRHVNILLFMGTWTKDNLAIVTQWCEGSSLYKHLHVQETK-FQMFQLIDIAROTAQGM DY 458
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 321 LKHDKLVLQLYAVVSEPIYIVTEYMNKGSLLDFLDKGEGRAIKLPNLVDMAAQVAAGMAY 380
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 459 LHAKNIIHRDMKSNIFLHEGLTVKIGDFGLATV--KSRWSGQQVEQPTGSLVWMAPEV 516
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 381 IERNMYIHRDLRSANILVGNGLICKIADFGLARLIEDNEYTARQAKFP---IKWTAPEA 437
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 517 IRMQDNNPFSQSDYISYGIYLYELMT-GELPYSHINNRDQIIFMVGRGYASPDLSKLYK 575
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 438 ALY---GRTFKSDVNSFGILLTELVTGKRVPGCMNNR-EVLEQVERGYRMP-----CPQ 489
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 576 NCPKAMKRLVADCVKVKKEERPLFPQILSSIE 607
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 490 DCPISLHELMHCKKDPPEPTFEYLSQSFLE 521
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 09:44:12 ; Search time 18 Seconds
(without alignments)
1059.225 Million cell updates/sec

Title: US-09-637-302C-2

Perfect score: 3413

Sequence: 1 MEHIQAWKTSINGFGPKDA.....AHTEDINACTLTTSPLRVF 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3413	100.0	648	1	US-08-276-151-2
2	3413	100.0	648	1	US-08-185-282-12
3	3413	100.0	648	2	US-08-886-751A-6
4	3413	100.0	648	3	US-09-209-668-13
5	3413	100.0	648	4	US-08-971-207-1
6	3331	97.6	648	1	US-08-185-282-3
7	3326	97.5	648	1	US-08-185-282-1
8	3325	97.4	648	1	US-08-185-282-2
9	3318	97.2	648	1	US-08-185-282-4
10	3299	96.7	648	1	US-08-185-282-5
11	1817	53.2	346	1	US-08-276-151-5
12	1641	48.1	315	1	US-08-571-758-12
13	1641	48.1	315	1	US-08-909-984A-12
14	1641	48.1	315	1	US-08-909-983-12
15	1373	40.2	257	1	US-08-077-256-1
16	1373	40.2	257	1	US-08-259-672-1
17	1373	40.2	257	1	US-08-459-351-1
18	1373	40.2	257	1	US-08-460-533-1
19	1373	40.2	257	5	PCT-US94-06654-1
20	1369	40.1	267	2	US-07-857-224B-42
21	1165	34.1	271	3	US-09-035-706-6
22	1165	34.1	271	3	US-08-955-841-6
23	1165	34.1	271	4	US-09-390-425-6
24	1165	34.1	271	4	US-09-566-906-6
25	1143	33.5	217	2	US-08-886-751A-5
26	1127.5	33.0	266	2	US-07-857-224B-43
27	1123	32.9	267	2	US-07-857-224B-45

28	1111.5	32.6	266	2	US-07-857-224B-44	Sequence 44, Appl
29	1071	31.4	197	1	US-08-276-151-3	Sequence 3, Appl1
30	1015	29.7	326	1	US-08-571-758-11	Sequence 11, Appl
31	1015	29.7	326	1	US-08-909-984A-11	Sequence 11, Appl
32	1015	29.7	326	1	US-08-909-983-11	Sequence 11, Appl
33	790	23.1	149	1	US-08-259-672-6	Sequence 6, Appl1
34	790	23.1	149	1	US-08-459-351-6	Sequence 6, Appl1
35	790	23.1	149	1	US-08-460-533-6	Sequence 6, Appl1
36	790	23.1	149	4	US-08-971-207-2	Sequence 2, Appl1
37	790	23.1	149	5	PCT-US94-06654-6	Sequence 2, Appl1
38	786	23.0	148	2	US-08-886-751A-4	Sequence 4, Appl1
39	753	22.1	147	1	US-08-276-151-4	Sequence 4, Appl1
40	753	16.8	966	1	US-08-571-758-2	Sequence 2, Appl1
41	575	16.8	966	1	US-08-909-984A-2	Sequence 2, Appl1
42	575	16.8	966	1	US-08-909-983-2	Sequence 2, Appl1
43	569.5	16.7	1003	1	US-08-571-758-4	Sequence 4, Appl1
44	569.5	16.7	1003	1	US-08-909-984A-4	Sequence 4, Appl1
45	569.5	16.7	1003	1	US-08-909-983-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-276-151-2
; Sequence 2, Application US/08276151
; Patent No. 5597719
; GENERAL INFORMATION:
; APPLICANT: Freed, Ellen
; APPLICANT: Ruggieri, Rosamaria
; TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward et al.
; STREET: Five Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,151
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: ONYX-005/0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5481
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-151-2

Query Match 100.0%; Score 3413; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHIQAWKTSINGFGKDAVFDGSSCISPTIVQQFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIQAWKTSINGFGKDAVFDGSSCISPTIVQQFGYQRRASDDGKLTDPKSTNTIRV 60
QY 61 FLNPKRTVVVNRNGMSLHDLCKALKVRGLQPECCAVFRLHHEHKGKRLDWNNTDAAS 120

Db 61 FLPNKRQTVVNVNRNGSLHDCLMKALKVRLQPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
Db 121 LIGELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
QY 181 PTCVDSNTRQLLLFPNSNIGSGVPALPSLWRRMRESVSRMPVSSQHRYSTPHFTF 240
Db 181 PTCVDSNTRQLLLFPNSNIGSGVPALPSLWRRMRESVSRMPVSSQHRYSTPHFTF 240
QY 241 NTSSPSEGSLSQRORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSUSPNNL 300
Db 241 NTSSPSEGSLSQRORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSUSPNNL 300
QY 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRGQDSSYYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRGQDSSYYWEIEASEVYMLSTRIGSGSF 360
QY 361 GTVYKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRKTRHVNILLFWMYTKDNLAI 420
Db 361 GTVYKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRKTRHVNILLFWMYTKDNLAI 420
QY 421 TQWCEGSSLYKHLHVQETKFMQLDIDARQTAQGMIDYLAHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQLDIDARQTAQGMIDYLAHAKNIHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSWSGSGQVQPTGSLVWMAPEVIRMQDNNPFSQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVKSWSGSGQVQPTGSLVWMAPEVIRMQDNNPFSQSDVYSYGVLYE 540
QY 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPRAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPRAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648

RESULT 2
US-08-185-282-12
; Sequence 12, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-185-282-12
Query Match 100.0%; Score 3413; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHIOGAKNTISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPSTKTSNIRV 60
Db 1 MEHIOGAKNTISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPSTKTSNIRV 60
QY 61 FLPNKRQTVVNVNRNGSLHDCLMKALKVRLQPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKRQTVVNVNRNGSLHDCLMKALKVRLQPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
Db 121 LIGELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
QY 181 PTCVDSNTRQLLLFPNSNIGSGVPALPSLWRRMRESVSRMPVSSQHRYSTPHFTF 240
Db 181 PTCVDSNTRQLLLFPNSNIGSGVPALPSLWRRMRESVSRMPVSSQHRYSTPHFTF 240
QY 241 NTSSPSEGSLSQRORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSUSPNNL 300
Db 241 NTSSPSEGSLSQRORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSUSPNNL 300
QY 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRGQDSSYYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRGQDSSYYWEIEASEVYMLSTRIGSGSF 360
QY 361 GTVYKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRKTRHVNILLFWMYTKDNLAI 420
Db 361 GTVYKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRKTRHVNILLFWMYTKDNLAI 420
QY 421 TQWCEGSSLYKHLHVQETKFMQLDIDARQTAQGMIDYLAHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQLDIDARQTAQGMIDYLAHAKNIHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSWSGSGQVQPTGSLVWMAPEVIRMQDNNPFSQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVKSWSGSGQVQPTGSLVWMAPEVIRMQDNNPFSQSDVYSYGVLYE 540
QY 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPRAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPRAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648

RESULT 3
US-08-886-751A-6
; Sequence 6, Application US/08886751A
; Patent No. 5885783
; GENERAL INFORMATION:
; APPLICANT: Yoo, Tai-June
; APPLICANT: Cheng, Kuang-Chuan
; TITLE OF INVENTION: Autoimmune Inner Ear Disease Antigen and
; TITLE OF INVENTION: Diagnostic Assay
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta

STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,751A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Young, Leona G.
REGISTRATION NUMBER: 37,266
REFERENCE/DOCKET NUMBER: 25490-0100
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

US-08-886-751A-6

Query Match 100.0%; Score 3413; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEHIOGAWKTIISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
DB 1 MEHIOGAWKTIISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFCQTCGKFKHEHCSTKV 180
DB 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFCQTCGKFKHEHCSTKV 180
QY 181 PTMCVDSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
DB 181 PTMCVDSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
QY 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
DB 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQREAPVSGTQENKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQREAPVSGTQENKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWGDVAVKILKVVDPTEQOFAFRNEAVLKRTHVNIILFMGYMTKDNLAIV 420
DB 361 GTVYKKGWGDVAVKILKVVDPTEQOFAFRNEAVLKRTHVNIILFMGYMTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTAQGMIDYLAHAKNIHRDMKSNIFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTAQGMIDYLAHAKNIHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWSSGQVEQPTGVLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRWSSGQVEQPTGVLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
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QY 541 LMTGELPYSHINNRODQIIFWVGRYGASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRODQIIFWVGRYGASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRVF 648
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RESULT 4

US-09-209-668-13
; Sequence 13, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-209-668-13

Query Match 100.0%; Score 3413; DB 3; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEHIOGAWKTIISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
DB 1 MEHIOGAWKTIISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFCQTCGKFKHEHCSTKV 180
DB 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFCQTCGKFKHEHCSTKV 180
QY 181 PTMCVDSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
DB 181 PTMCVDSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
QY 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
DB 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQREAPVSGTQENKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQREAPVSGTQENKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWGDVAVKILKVVDPTEQOFAFRNEAVLKRTHVNIILFMGYMTKDNLAIV 420
DB 361 GTVYKKGWGDVAVKILKVVDPTEQOFAFRNEAVLKRTHVNIILFMGYMTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTAQGMIDYLAHAKNIHRDMKSNIFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTAQGMIDYLAHAKNIHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWSSGQVEQPTGVLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRWSSGQVEQPTGVLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
QY 541 LMTGELPYSHINNRODQIIFWVGRYGASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRODQIIFWVGRYGASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
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QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 5
US-08-971-207-1
; Sequence 1, Application US/08971207
; Patent No. 6300081
; GENERAL INFORMATION:
; APPLICANT: Taylor, Stephen J.
; APPLICANT: Shalloway, David
; TITLE OF INVENTION: ACTIVATED RAS INTERACTION ASSAY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/971,207
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,924
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-971-207-1

Query Match 100.0%; Score 3413; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHIQGAWKTSINGFGKDAVFGDSSCISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIQGAWKTSINGFGKDAVFGDSSCISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60
QY 61 FLNPKQRTVVNVNRMGSLHDCLMKALKVRGLQPECCAVFRLLEHKKARLDWNTDAAS 120
Db 61 FLNPKQRTVVNVNRMGSLHDCLMKALKVRGLQPECCAVFRLLEHKKARLDWNTDAAS 120
QY 121 LIGEELOVDLHDVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKKEHCSTKV 180
Db 121 LIGEELOVDLHDVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKKEHCSTKV 180
QY 181 PTMCDVMSNRQLLFPNSTIGSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHFTF 240
Db 181 PTMCDVMSNRQLLFPNSTIGSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHFTF 240
QY 241 NTSSPSSEGLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNL 300
Db 241 NTSSPSSEGLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNL 300

QY 301 SPTGWSQKTPVPAQRERAPVSGTOEKNKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTOEKNKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKGRWHGDAVAVKILKVVDPTPEQFOAFNEAVLRKTHVNLILFMGYMTKDNLAIV 420
Db 361 GTVYKGRWHGDAVAVKILKVVDPTPEQFOAFNEAVLRKTHVNLILFMGYMTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFOFQOLIDIAROTAGQMDYLHAKNIIHRDMKSNNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFOFQOLIDIAROTAGQMDYLHAKNIIHRDMKSNNIFLHEGL 480
QY 481 TVKIGDFGLATVYKRWGSGSQVEQPTGSLVMAPEVIRMODNNPFSQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVYKRWGSGSQVEQPTGSLVMAPEVIRMODNNPFSQSDVYSYGVLYE 540
QY 541 LMTGELPYSHINNRRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 6
US-08-185-282-3
; Sequence 3, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-185-282-3

Query Match 97.6%; Score 3331; DB 1; Length 648;
Best Local Similarity 97.5%; Pred. No. 2.5e-286;
Matches 632; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 MEHIQGAWKTSINGFGKDAVFGDSSCISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60


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Db 1 MEHIQAWKTSNGFGLKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDSSTNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPITTHNFARKTFLKLAFCDCQKFLNGFRQCOTCGYKFEHCSTKV 180
Db 121 LIGELQVDFLDHVPITTHNFARKTFLKLAFCDCQKFLNGFRQCOTCGYKFEHCSTKV 180
QY 181 PTMCVDWSNIRQLLFPNSTIGDSGVPALPSLTHRMRESVSRMPVSSQHRYSSTPHAFTE 240
Db 181 PTMCVDWSNIRQLLFPNSTIGDSGVPALPSLTHRMRESVSRMPVSSQHRYSSTPHAFTE 240
QY 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLVDSRMIEDAIRSHSESASPSALSSSPNNL 300
Db 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLVDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQRERAPVSGTOEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTOEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQQAERNEVAVLRKTRHVNILLFMGYMTKDLAIV 420
Db 361 GTVYKKGWHDVAVKILKVVDPTPEQQAERNEVAVLRKTRHVNILLFMGYMTKDLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKQFQMLIDIAQOTAGMDYLHAKNIITHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKQFQMLIDIAQOTAGMDYLHAKNIITHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWGSQVEQPTGSLVLMWMAPEVIRMQDNNPFSQSDVYSYGIYLVE 540
Db 481 TVKIGDFGLATVKSRWGSQVEQPTGSLVLMWMAPEVIRMQDNNPFSQSDVYSYGIYLVE 540
QY 541 LMTGELPYSHINNROQIIFWVGRIYASPDLSKLYKNCPRKMLRVADCVKKEERPLFP 600
Db 541 LMTGELPYSHINNROQIIFWVGRIYASPDLSKLYKNCPRKMLRVADCVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
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RESULT 7

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US-08-185-282-1
; Sequence 1, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
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; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-185-282-1
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Query Match 97.5%; Score 3326; DB 1; Length 648;
Best Local Similarity 97.4%; Pred. No. 6.9e-286;
Matches 631; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
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QY 1 MEHIQAWKTSNGFGLKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDSSTNTIRV 60
Db 1 MEHIQAWKTSNGFGLKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDSSTNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPITTHNFARKTFLKLAFCDCQKFLNGFRQCOTCGYKFEHCSTKV 180
Db 121 LIGELQVDFLDHVPITTHNFARKTFLKLAFCDCQKFLNGFRQCOTCGYKFEHCSTKV 180
QY 181 PTMCVDWSNIRQLLFPNSTIGDSGVPALPSLTHRMRESVSRMPVSSQHRYSSTPHAFTE 240
Db 181 PTMCVDWSNIRQLLFPNSTIGDSGVPALPSLTHRMRESVSRMPVSSQHRYSSTPHAFTE 240
QY 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLVDSRMIEDAIRSHSESASPSALSSSPNNL 300
Db 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLVDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQRERAPVSGTOEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
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QY 361 GTVYKKGWHDVAVKILKVVDPTPEQQAERNEVAVLRKTRHVNILLFMGYMTKDLAIV 420
Db 361 GTVYKKGWHDVAVKILKVVDPTPEQQAERNEVAVLRKTRHVNILLFMGYMTKDLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKQFQMLIDIAQOTAGMDYLHAKNIITHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKQFQMLIDIAQOTAGMDYLHAKNIITHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWGSQVEQPTGSLVLMWMAPEVIRMQDNNPFSQSDVYSYGIYLVE 540
Db 481 TVKIGDFGLATVKSRWGSQVEQPTGSLVLMWMAPEVIRMQDNNPFSQSDVYSYGIYLVE 540
QY 541 LMTGELPYSHINNROQIIFWVGRIYASPDLSKLYKNCPRKMLRVADCVKKEERPLFP 600
Db 541 LMTGELPYSHINNROQIIFWVGRIYASPDLSKLYKNCPRKMLRVADCVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
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RESULT 8

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US-08-185-282-2
; Sequence 2, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
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Db 241 NTSSPSSEGLSQRORSTSTPNVHMVSTTLRVDSRMIEDAIRSHSESASPSALSSPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGORDSSYYWIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGORDSSYYWIEASEVMLSTRIGSGSF 360
Qy 361 GTVYKGKHWGDVAVKILKVVDPTPEQQAQFNEVAVLRKTRHVNILLFMCYMTKDNLAIV 420
Db 361 GTVYKGKHWGDVAVKILKVVDPTPEQQAQFNEVAVLRKTRHVNILLFMCYMTKDNLAIV 420
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Db 421 TQWCEGSSLYKHLHVQETKQFQDLIDIAQOTAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQVQEQPTGSLWMAPEVIRMQDNNPFSQSDVYSGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQVQEQPTGSLWMAPEVIRMQDNNPFSQSDVYSGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIellohslpklnrsasepslhraahtedinactlttsprlpvf 648
Db 601 QILSSIellohslpklnrsasepslhraahtedinactlttsprlpvf 648
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RESULT 10

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US-08-185-282-5
; Sequence 5, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-185-282-5
Query Match 96.7%; Score 3299; DB 1; Length 648;
Best Local Similarity 96.8%; Pred. No. 1.7e-283;
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Matches 627; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
Qy 1 MEHIOGAWKTIISNGFGFKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIOGAWKTIISNGFGFKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60
Qy 61 FLPNKQRTVYVNRNGMSLHDCLMKALKVRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120
Db 61 FLPNKQRTVYVNRNGMSLHDCLMKALKVRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120
Qy 121 LGEELOVDFLDHVPITTHNFARKTFLKAFCDICOKFLNLFRCOTCGYKFEHCSTKV 180
Db 121 LGEELOVDFLDHVPITTHNFARKTFLKAFCDICOKFLNLFRCOTCGYKFEHCSTKV 180
Qy 181 PTMCDVWSNIRQLLFPNSTIGDSVGPALPSITMRMRRESVSRMPVSSOHRVSTPHATTF 240
Db 181 PTMCDVWSNIRQLLFPNSTIGDSVGPALPSITMRMRRESVSRMPVSSOHRVSTPHATTF 240
Qy 241 NTSSPSSEGLSQRORSTSTPNVHMVSTTLRVDSRMIEDAIRSHSESASPSALSSPNNL 300
Db 241 NTSSPSSEGLSQRORSTSTPNVHMVSTTLRVDSRMIEDAIRSHSESASPSALSSPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGORDSSYYWIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGORDSSYYWIEASEVMLSTRIGSGSF 360
Qy 361 GTVYKGKHWGDVAVKILKVVDPTPEQQAQFNEVAVLRKTRHVNILLFMCYMTKDNLAIV 420
Db 361 GTVYKGKHWGDVAVKILKVVDPTPEQQAQFNEVAVLRKTRHVNILLFMCYMTKDNLAIV 420
Qy 421 TQWCEGSSLYKHLHVQETKQFQDLIDIAQOTAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKQFQDLIDIAQOTAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQVQEQPTGSLWMAPEVIRMQDNNPFSQSDVYSGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQVQEQPTGSLWMAPEVIRMQDNNPFSQSDVYSGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIellohslpklnrsasepslhraahtedinactlttsprlpvf 648
Db 601 QILSSIellohslpklnrsasepslhraahtedinactlttsprlpvf 648
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RESULT 11

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US-08-276-151-5
; Sequence 5, Application US/08276151
; Patent No. 5597719
; GENERAL INFORMATION:
; APPLICANT: Freed, Ellen
; APPLICANT: Ruggieri, Rosamaria
; TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward et al.
; STREET: Five Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,151
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/909,984A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: B96-010
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 315 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-909-984A-12

Query Match 48.1%; Score 1641; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 3.5e-137;
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 334 GORDSSYYWEIEASEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTPEQFAFRNE 393
Db 1 GORDSSYYWEIEASEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTPEQFAFRNE 60
Qy 394 VAVLRKTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFLIDIAQTA 453
Db 61 VAVLRKTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFLIDIAQTA 120
Qy 454 QGMDYLHAKNIIHRDKMKNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVWMA 513
Db 121 QGMDYLHAKNIIHRDKMKNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVWMA 180
Qy 514 PEVIRMODNPNFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKL 573
Db 181 PEVIRMODNPNFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKL 240
Qy 574 YKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTED 633
Db 241 YKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTED 300
Qy 634 INACTLTTSPLPVPF 648
Db 301 INACTLTTSPLPVPF 315

RESULT 14
US-08-909-983-12
; Sequence 12, Application US/08909983
; Patent No. 5747288
; GENERAL INFORMATION:
; APPLICANT: Rublin, Gerry M.
; APPLICANT: Therrien, Marc
; APPLICANT: Chang, Henry C.
; APPLICANT: Karim, Felix D.
; APPLICANT: Wasserman, David A.
; TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
; TITLE OF INVENTION: Signal transduction
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/909,983
;; FILING DATE: 12-JUN-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/571,758
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: B96-010
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 315 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-909-983-12

Query Match 48.1%; Score 1641; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 3.5e-137;
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 334 GORDSSYYWEIEASEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTPEQFAFRNE 393
Db 1 GORDSSYYWEIEASEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTPEQFAFRNE 60
Qy 394 VAVLRKTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFLIDIAQTA 453
Db 61 VAVLRKTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFLIDIAQTA 120
Qy 454 QGMDYLHAKNIIHRDKMKNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVWMA 513
Db 121 QGMDYLHAKNIIHRDKMKNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVWMA 180
Qy 514 PEVIRMODNPNFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKL 573
Db 181 PEVIRMODNPNFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKL 240
Qy 574 YKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTED 633
Db 241 YKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTED 300
Qy 634 INACTLTTSPLPVPF 648
Db 301 INACTLTTSPLPVPF 315

RESULT 15
US-08-077-256-1
; Sequence 1, Application US/08077256
; Patent No. 5582995
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch, M.D.
; APPLICANT: Xian-feng Zhang, Ph.D.
; TITLE OF INVENTION: INHIBITING PROTEIN
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 555X

;; OPERATING SYSTEM: MS-DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/077,256
;; FILING DATE: 19930611
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Paul T. Clark, Esq.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 00786/190001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 257
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
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Us-08-077-256-1

Query Match 40.2%; Score 1373; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.4e-113;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 61 FLPNKQRTVVNVNRMGSLHDCLMKALKVRGLQPECCAVFRLLEHKGKARKLDWNTDAAS 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 FLPNKQRTVVNVNRMGSLHDCLMKALKVRGLQPECCAVFRLLEHKGKARKLDWNTDAAS 120
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QY 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKFHEHCSTKV 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKFHEHCSTKV 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 PTMCVDWSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSOHRYSTPHFTTF 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 PTMCVDWSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSOHRYSTPHFTTF 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 241 NTSSPSSEGSLSQQRQS 257
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: July 9, 2003, 09:47:06
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:35:32 ; Search time 41 seconds
(without alignments)
2106.010 Million cell updates/sec

Title: US-09-637-302c-2

Perfect score: 3413

Sequence: 1 MEHIQAWKTIISNGFGKDA.....AHTEDINACTLTSPRLPVF 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3413	100.0	648	18	AA17044 Human c-raf 1 prot
3	3413	100.0	648	18	AA17044 Human Raf-1. Homo
4	3413	100.0	648	19	AA17044 Human Raf-1. Homo
5	3413	100.0	648	20	AA17044 Human Raf-1. Homo
6	3413	100.0	648	20	AA17044 Homo sapiens GSR-R
7	3413	100.0	648	21	AA17044 Human c-raf-1 prot
8	3413	100.0	648	21	AA17044 Human ORF2465
9	3413	100.0	648	21	AA17044 Human c-raf protel
10	3413	100.0	648	22	AA170295 Human c-Raf protel

11	3413	100.0	648	22	AA17044 Amino acid sequenc
12	3413	100.0	648	22	AA17044 Amino acid sequenc
13	3413	100.0	648	23	AA17044 Human protein kina
14	3413	100.0	648	23	AA17044 Human c-raf-1 prot
15	3413	100.0	648	23	AA17044 Raf-1 fusion pr
16	3406	99.8	648	13	AA17044 Human c-raf-1. Ho
17	3379	99.0	648	20	AA17044 Human c-raf-1 prot
18	3331	97.6	648	18	AA17044 Mutant mouse c-raf
19	3331	97.6	648	20	AA17044 Mutant mouse c-raf
20	3326	97.5	648	13	AA17044 Mouse c-raf-1. Mu
21	3326	97.5	648	18	AA17044 Mouse c-raf-1 prot
22	3325	97.5	648	20	AA17044 Mouse c-raf-1 prot
23	3325	97.4	648	18	AA17044 Mutant mouse c-raf
24	3325	97.4	648	20	AA17044 Mutant mouse c-raf
25	3318	97.2	648	18	AA17044 Mutant mouse c-raf
26	3318	97.2	648	20	AA17044 Mutant mouse c-raf
27	3311	97.0	648	13	AA17044 Mouse mutant c-raf
28	3305	96.8	648	13	AA17044 Mouse mutant c-raf
29	3305	96.8	648	13	AA17044 Mouse mutant c-raf
30	3299	96.7	648	18	AA17049 Mouse mutant c-raf
31	3299	96.7	648	20	AA17049 Mouse mutant c-raf
32	3278	96.0	648	13	AA17049 Mouse mutant c-raf
33	1889.5	55.4	606	23	AA17049 Mouse mutant c-raf
34	1882.5	55.2	606	23	AA17049 Mouse mutant c-raf
35	1825	53.5	765	23	AA17049 Human protein kina
36	1823.5	53.4	650	13	AA17049 Human protein kina
37	1384	40.6	739	22	AA17049 Human B-raf protei
38	1373	40.2	257	16	AA17049 Drosophila melanog
39	1373	40.2	257	19	AA17049 Raf(1-257) oncopro
40	1373	40.2	257	19	AA17049 Ras-binding fragme
41	1369	40.1	267	20	AA17049 Ras-binding fragme
42	1277	37.4	516	12	AA17049 Yeast protein kina
43	1277	37.4	516	12	AA17049 Sequence encoded b
44	1143	33.5	217	20	AA17049 T18 oncogene prod.
45	1143	33.5	217	21	AA17049 Homo sapiens GSR-R
					Amino acid sequenc

ALIGNMENTS

RESULT 1

AA198215

ID AA198215 standard; Protein; 648 AA.

XX AA198215;

XX AC AA198215;

XX DT 24-SEP-1996 (first entry)

XX DE Human Raf1 kinase.

XX KW CDC25; phosphatase; Raf protein; proliferative disorder; cancer;
XX KW leukemia; psoriasis; bone disorder; fibroproliferative disorders;
XX KW differentiation associated disorder; kinase;
XX KW chronic neurodegenerative disease; vascular disorder.

XX OS Homo sapiens.

XX PN WO9612820-A1.

XX PD 02-MAY-1996.

XX PF 23-OCT-1995; 95WO-US13661.

XX PR 24-OCT-1994; 94US-0328239.

XX PA (COLD-) COLD SPRING HARBOR LAB.

XX PI Beach DH, Galaktionov K, Jessus C;

XX DR WPI; 1996-230619/23.

XX DR N-PSDB; AAT30085.

XX PT Identification of cpds. which modulate and inhibit ras-mediated

PT activation of CDC25 - useful in treatment of proliferative disorders
PT and differentiation associated disorders, e.g. chronic
PT neurodegenerative diseases

XX Claim 14; Page 44-47; 52pp; English.

XX CDC25 phosphatases (e.g. AAT30082-T30084) and Raf proteins (e.g.
CC AAT30085) are able to physically interact to form protein-protein
CC complexes, with the Raf protein mediating the activation of CDC25
CC phosphatases. Modulators and inhibitors of ras-mediated CDC25
CC activation and modulators and inhibitors of interaction between
CC CDC25 phosphatase and Raf-kinase can be used in the treatment
CC of proliferative disorders, e.g. cancers, leukemias, psoriasis,
CC bone disorders, fibroproliferative disorders, differentiation
CC associated disorders, e.g. chronic neurodegenerative diseases,
CC vascular disorders and disorders associated with degenerative
CC changes in glandular cells and the inhibition of spermatogenesis.

XX SQ Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 17; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTIISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIQAWKTIISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLNPKORTVNVNRGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
DB 61 FLNPKORTVNVNRGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGEEQVDFLDHVPVLTTHNFARKTEKLFKAFCDICQKFLNGFRQTCGKFEHCSTKV 180
DB 121 LIGEEQVDFLDHVPVLTTHNFARKTEKLFKAFCDICQKFLNGFRQTCGKFEHCSTKV 180
QY 181 PTMCDVWSNIRQLLLFPNSTIGDGVGVPALPSLTMRRRESVSRMPVSSQHRYSSTPHAF 240
DB 181 PTMCDVWSNIRQLLLFPNSTIGDGVGVPALPSLTMRRRESVSRMPVSSQHRYSSTPHAF 240
QY 181 PTMCDVWSNIRQLLLFPNSTIGDGVGVPALPSLTMRRRESVSRMPVSSQHRYSSTPHAF 240
DB 181 PTMCDVWSNIRQLLLFPNSTIGDGVGVPALPSLTMRRRESVSRMPVSSQHRYSSTPHAF 240
QY 241 NTSSPSSGSLSQORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPALSPPNNL 300
DB 241 NTSSPSSGSLSQORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPALSPPNNL 300
QY 301 SPTGWSQKTPVPAQERAPVSGTQEKNIIRPRGQRRDSSYYWEIEASEVYMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQERAPVSGTQEKNIIRPRGQRRDSSYYWEIEASEVYMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMYTKDLNLAIV 420
DB 361 GTVYKKGWHDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMYTKDLNLAIV 420
QY 421 TQCEGSSLYKHLHVQETKQFQMLIDIAQTAQGMIDYLAHAKNIIRHDKSNIFLHEGL 480
DB 421 TQCEGSSLYKHLHVQETKQFQMLIDIAQTAQGMIDYLAHAKNIIRHDKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRSQSGVQEPQGSVLWMAPEVIRMQDNNPFSQSDVYSYGLVLYE 540
DB 481 TVKIGDFGLATVKSRSQSGVQEPQGSVLWMAPEVIRMQDNNPFSQSDVYSYGLVLYE 540
QY 541 LMTGELPYSHINNRDQIIFVWGRGYASPDLSKLYKNCPRKMLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRDQIIFVWGRGYASPDLSKLYKNCPRKMLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLQHSPLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
DB 601 QILSSIELLQHSPLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 2

AAW17044

ID AAW17044 standard; Protein; 648 AA.

XX

AC AAW17044;
XX 07-JUL-1997 (first entry)
DT Human c-raf 1 protein used in diagnosis of lymphoma or lung cancer.
DE
XX
XX raf; oncogene; lymphoma; lung cancer; neoplasia; point mutation;
KW conserved region; adenocarcinoma; codon 533; diagnosis; detection.
XX
XX Homo sapiens.
XX US5618670-A.
PN 08-APR-1997.
PD 26-AUG-1988; 88US-0236947.
PF 16-SEP-1991; 91US-0759738.
PR 26-AUG-1988; 88US-0236947.
PR 24-JAN-1994; 94US-0185282.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rapp UR, Storm SM;

XX WPI; 1997-225421/20.

DR N-PSDB; AAT68800.

XX Classification of lymphoma or lung cancer - on the basis of a point mutation in c-raf-1 gene

XX Claim 2; Column 35-38; 26pp; English.

XX AAW17044, the human c-raf-1 protein, was used in a method for classifying a lymphoma or lung cancer in an individual. The method involves detecting the presence of a point mutation in a conserved region of the c-raf-1 gene (codon 533, encoding Ser, in this sequence) derived from lymphoma or lung cancer tissue and classifying the lymphoma or lung cancer as a c-raf-1 mutation-associated cancer if one or more point mutations are present. The method is particularly applicable to lung adenocarcinoma.

XX SQ Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 18; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTIISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIQAWKTIISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLNPKORTVNVNRGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
DB 61 FLNPKORTVNVNRGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGEEQVDFLDHVPVLTTHNFARKTEKLFKAFCDICQKFLNGFRQTCGKFEHCSTKV 180
DB 121 LIGEEQVDFLDHVPVLTTHNFARKTEKLFKAFCDICQKFLNGFRQTCGKFEHCSTKV 180
QY 181 PTMCDVWSNIRQLLLFPNSTIGDGVGVPALPSLTMRRRESVSRMPVSSQHRYSSTPHAF 240
DB 181 PTMCDVWSNIRQLLLFPNSTIGDGVGVPALPSLTMRRRESVSRMPVSSQHRYSSTPHAF 240
QY 241 NTSSPSSGSLSQORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPALSPPNNL 300
DB 241 NTSSPSSGSLSQORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPALSPPNNL 300
QY 301 SPTGWSQKTPVPAQERAPVSGTQEKNIIRPRGQRRDSSYYWEIEASEVYMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQERAPVSGTQEKNIIRPRGQRRDSSYYWEIEASEVYMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMYTKDLNLAIV 420

Db 361 GTVYKRGHGDVAVKILKVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYTKDNLAI 420
QY 421 TQWCEGSSLYKHLHVQETKFMOLFIDIAOTAGMDYLHAKNIHHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMOLFIDIAOTAGMDYLHAKNIHHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWSGQVEQPTGSLVWMAPEVIRMDQNNPFQSDVYSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWSGQVEQPTGSLVWMAPEVIRMDQNNPFQSDVYSYGIVLYE 540
QY 541 LMTGELPYSHNNRQDIIFMVGGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHNNRQDIIFMVGGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIellohSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIellohSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648

RESULT 3
AAW13107
ID AAW13107 standard; Protein; 648 AA.
AC AAW13107;
XX
DT 12-MAY-1997 (first entry)
DE Human Raf-1.
XX
KW Human; raf-1; complex; 14-3-3; beta; zeta; modulation; binding;
KW detection; screening; interaction; cell cycle; control; neoplasia;
KW pathological condition; drug.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT 1..197
FT /note= "conserved region 1 containing region"
FT 186..332
FT /note= "conserved region 2 containing region"
XX
US5597719-A.
XX
XX 28-JAN-1997.
XX
XX 14-JUL-1994; 94US-0276151.
XX
XX 14-JUL-1994; 94US-0276151.
XX
XX (ONYX-) ONYX PHARM INC.
XX
PI Freed E, Ruggieri R;
XX
XX WPI; 1997-108327/10.
XX
XX N-PSDB; AAT61894.
XX
XX Complex of raf-1 and 14-3-3 polypeptide(s) - useful for anticancer
XX drug screening
XX
XX Disclosure; Columns 31-38; 43pp; English.
XX
XX The present sequence is human Raf-1, which can be used in a
XX novel composition comprising a complex of human Raf-1, or a
XX fragment comprising residues 1-197 or 186-332, or lacking residues
XX 51-131, and a 14-3-3 polypeptide (preferably human 14-3-3 beta or
XX zeta). The composition can be used to screen for drugs which
XX modulate the binding interaction between Raf-1 and 14-3-3,
XX especially to identify drugs that modulate Raf-1 mediated cell
XX cycle control, and/or neoplastic or other pathological conditions
XX dependent on the interaction between Raf-1 and 14-3-3 beta or zeta.
XX
XX Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 18; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHIQGAWKTSINGFGFKDAVFDGSGSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIQGAWKTSINGFGFKDAVFDGSGSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
QY 61 FLNPKQRTVYVNRNGSLHDCLMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLNPKQRTVYVNRNGSLHDCLMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGBELQVDFLDHVPLTTHNFARKTFELKLAFCIDICOKFLNGFRCTCGVKFHEHCSTKV 180
Db 121 LIGBELQVDFLDHVPLTTHNFARKTFELKLAFCIDICOKFLNGFRCTCGVKFHEHCSTKV 180
QY 181 PTMCVMSNTRQQLLLFPNSTIGDGVPAALPSLTPMRRRESVSRRMPVSSQHRYSTPHATTF 240
Db 181 PTMCVMSNTRQQLLLFPNSTIGDGVPAALPSLTPMRRRESVSRRMPVSSQHRYSTPHATTF 240
QY 241 NTSSPSEGLSORQSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSEGLSORQSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
QY 301 SPTGWSQKTPVPAQRERAPVSGTQKKNIRPGQDSSYIWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTQKKNIRPGQDSSYIWEIEASEVYMLSTRIGSGSF 360
QY 361 GTVYKRGHGDVAVKILKVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYTKDNLAI 420
Db 361 GTVYKRGHGDVAVKILKVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYTKDNLAI 420
QY 421 TQWCEGSSLYKHLHVQETKFMOLFIDIAOTAGMDYLHAKNIHHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMOLFIDIAOTAGMDYLHAKNIHHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWSGQVEQPTGSLVWMAPEVIRMDQNNPFQSDVYSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWSGQVEQPTGSLVWMAPEVIRMDQNNPFQSDVYSYGIVLYE 540
QY 541 LMTGELPYSHNNRQDIIFMVGGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHNNRQDIIFMVGGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIellohSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIellohSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648

RESULT 4
AAW62220
ID AAW62220 standard; protein; 648 AA.
XX
XX AAW62220;
XX
XX AC AAW62220;
XX
XX DT 17-SEP-1998 (first entry)
XX
XX DE Raf-1 protein.
XX
XX KW ras binding domain; raf-1; ras interaction assay; detection; diagnosis;
XX KW activated; oncogene; malignant; human; cancer; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN W09821585-A1.
XX
XX PD 22-MAY-1998.
XX
XX PF 14-NOV-1997; 97WO-US21351.
XX
XX PR 15-NOV-1996; 96US-0030924.
XX

PA	(CORR) CORNELL RES FOUND INC.	
XX	Shalloway D, Taylor SJ;	
XX	WPI; 1998-298109/26.	
XX	Detecting activated ras protein from capture by immobilised protein	
PT	- having ras-binding domain, used for diagnosis and prognosis of	
PT	cancers involving mutated ras genes	
XX		
XX	Disclosure; Page 10-12; 47pp; English.	
XX		
CC	A method has been developed for detecting activated ras protein (I).	
CC	The method comprises: (i) immobilising a protein (II) containing a	
CC	ras-binding domain on a support; (ii) incubating (II) with	
CC	(I)-containing lysate from cultured cells, and (iii) determining	
CC	amount of (I) bound to (II). The present sequence represents a	
CC	raf-1 protein from the present invention. The method is used for	
CC	diagnosis and prognosis of malignancies (e.g. cancer of breast, colon,	
CC	lung or pancreas, also some forms of leukemia) related to (I) in	
CC	humans, i.e. where a mutation in a ras gene causes constitutive	
CC	activation. It may also be used to study normal regulation of (I) and	
CC	to evaluate compounds for activation of (I) in cultured cells. The	
CC	method: (i) does not require pretreatment of samples with radioisotopes,	
CC	so can be used to measure activation levels in whole tissue samples;	
CC	(ii) can detect specifically any of the individual ras isoforms, or all	
CC	forms collectively, and (iii) can detect all potential activating	
CC	mutations or activation in response to activation of other oncogenes.	
XX		
XX	Sequence 648 AA;	
XX	Query Match 100.0%; Score 3413; DB 19; Length 648;	
XX	Best Local Similarity 100.0%; Pred. No. 1.1e-298;	
XX	Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MEHIQAWKTSINGFGFKDAVFDGSSCISPTIVQOFGYORRASDDCKLTDPSKTSNTIRV 60	
Db	1 MEHIQAWKTSINGFGFKDAVFDGSSCISPTIVQOFGYORRASDDCKLTDPSKTSNTIRV 60	
Qy	61 FLPNKQRTVVVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEKGGKARLDWNTDAAS 120	
Db	61 FLPNKQRTVVVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEKGGKARLDWNTDAAS 120	
Qy	121 LIGELQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRQCQCYKFHEHCSTKV 180	
Db	121 LIGELQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRQCQCYKFHEHCSTKV 180	
Qy	181 PTMCVDSNIRQLLLFPNSTIGDGVPPALPSLTMRRRESVSRMPVSSQHRYSTPHAFTF 240	
Db	181 PTMCVDSNIRQLLLFPNSTIGDGVPPALPSLTMRRRESVSRMPVSSQHRYSTPHAFTF 240	
Qy	241 NTSSPSEGSLSQRSTSTPNVHMVSTTLFVDSRMIEDAIRSHSESASPSALSPPNML 300	
Db	241 NTSSPSEGSLSQRSTSTPNVHMVSTTLFVDSRMIEDAIRSHSESASPSALSPPNML 300	
Qy	301 SPTGWSOPKTPVAQREARVPSTQENKIRPRGORDSSVYWEIEASEVNLSPRIGSGSF 360	
Db	301 SPTGWSOPKTPVAQREARVPSTQENKIRPRGORDSSVYWEIEASEVNLSPRIGSGSF 360	
Qy	361 GTVYKGKWDGDAVKILKVVDPTPEQFQAFRNEVAVLRTKRVNILLFMGYMTKDLNLAIV 420	
Db	361 GTVYKGKWDGDAVKILKVVDPTPEQFQAFRNEVAVLRTKRVNILLFMGYMTKDLNLAIV 420	
Qy	421 TQWCEGSSLYKHLHVQTKQFQIDIAQRTAQGMIDYLAHAKNIIRDMSKNINIFLHEGL 480	
Db	421 TQWCEGSSLYKHLHVQTKQFQIDIAQRTAQGMIDYLAHAKNIIRDMSKNINIFLHEGL 480	
Qy	481 TVKIGDGLATVKSRRSGSQVQPTGSLVWMAPEVIRMDNNPFSQSDVTSYGLVLYE 540	
Db	481 TVKIGDGLATVKSRRSGSQVQPTGSLVWMAPEVIRMDNNPFSQSDVTSYGLVLYE 540	
Qy	541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600	
Db	541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600	
Db	541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600	
Qy	601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648	
Db	601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648	
Db	601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648	
RESULT 5		
AAW95611		
ID	AAW95611 standard; peptide; 648 AA.	
XX		
AC	AAW95611;	
XX		
DT	08-JUN-1999 (first entry)	
XX		
DE	Homo sapiens GST-Raf-1 protein.	
XX		
KW	Inner ear; 28kD antigen; Meniere's disease; membranous structure;	
KW	autoimmune disease; immunotherapy; Raf-1 protein.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9901085-A2.	
XX		
PD	14-JAN-1999.	
XX		
XX	01-JUL-1998; 98WO-US13796.	
PF		
XX		
PR	02-JUL-1997; 97US-0886751.	
XX		
PA	(CHEN/) CHENG K.	
PA	(YOOT/) YOO T.	
XX		
PI	Cheng K, Yoo T;	
XX		
XX	WPI; 1999-105735/09.	
XX		
XX	A new antigen of the inner ear membranous structure - useful to	
PT	diagnose Meniere's disease	
XX		
PS	Disclosure; Page 26-30; 38pp; English.	
XX		
CC	The sequence is that of a Raf-1 N-terminal fragment which was used	
CC	in the production of a 28kD antigen from the membranous structure	
CC	of the inner ear (ME antigen), reactive with antibodies from	
CC	patients having Meniere's disease. It can be used as part of a	
CC	method of detecting Meniere's disease in an animal or human and	
CC	to distinguish Meniere's disease from other autoimmune inner ear	
CC	diseases, to monitor the disease progression and effects of	
CC	treatment, and to provide an antigen for immunotherapeutic	
CC	treatment of the disease.	
XX		
SQ	Sequence 648 AA;	
	Query Match 100.0%; Score 3413; DB 20; Length 648;	
	Best Local Similarity 100.0%; Pred. No. 1.1e-298;	
	Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MEHIQAWKTSINGFGFKDAVFDGSSCISPTIVQOFGYORRASDDCKLTDPSKTSNTIRV 60	
Db	1 MEHIQAWKTSINGFGFKDAVFDGSSCISPTIVQOFGYORRASDDCKLTDPSKTSNTIRV 60	
Qy	61 FLPNKQRTVVVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEKGGKARLDWNTDAAS 120	
Db	61 FLPNKQRTVVVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEKGGKARLDWNTDAAS 120	
Qy	121 LIGELQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRQCQCYKFHEHCSTKV 180	
Db	121 LIGELQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRQCQCYKFHEHCSTKV 180	
Qy	181 PTMCVDSNIRQLLLFPNSTIGDGVPPALPSLTMRRRESVSRMPVSSQHRYSTPHAFTF 240	
Db	181 PTMCVDSNIRQLLLFPNSTIGDGVPPALPSLTMRRRESVSRMPVSSQHRYSTPHAFTF 240	

QY 241 NTSSPSSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSPPNNL 300
DB 241 NTSSPSSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSPPNNL 300
QY 301 SPTGNSQPTVPVPAQRERAPVSGTQEKNIIRPRGORDSSYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGNSQPTVPVPAQRERAPVSGTQEKNIIRPRGORDSSYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWGDVAVKTLKVVDPTEQFQAFRNEVAVLRKTRHVNILLFMGYMTKONLAIV 420
DB 361 GTVYKKGWGDVAVKTLKVVDPTEQFQAFRNEVAVLRKTRHVNILLFMGYMTKONLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRSWGSQQVEQPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIYLYE 540
DB 481 TVKIGDFGLATVKSRSWGSQQVEQPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIYLYE 540
QY 541 LMTGELPYSHINNROQIIFWVGRCYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNROQIIFWVGRCYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 6

AAW30664
ID AAW30664 standard; Protein; 648 AA.

XX AAW30664;

AC AAW30664;

DT 08-APR-1999 (first entry)

DE Human c-raf-1 protein.

XX Human; c-raf-1; oncogene; cancer; lung adenocarcinoma.

XX Homo sapiens.

XX US5869308-A.

XX 09-FEB-1999.

XX 01-APR-1997; 97US-0831317.

XX 16-SEP-1991; 91US-0759738.

XX 26-AUG-1988; 88US-0236947.

XX 24-JAN-1994; 94US-0185282.

XX 01-APR-1997; 97US-0831317.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rapp UR, Storm SM;

XX WPI; 1999-152776/13.

XX N-PSDB; AAX03925.

PT New isolated human nucleic acid unique to c-raf-1 - having a point

PT mutation in the conserved region encoding amino acids 450-630 of a

PT 648 amino acid sequence

XX Claim 1; Column 35-38; 26pp; English.

XX The present sequence represents human c-raf-1. The present invention

CC describes c-raf-1 having a point mutation in the conserved region

CC encoding amino acids 450-630 (preferably amino acid 533) of the human

CC c-raf-1 protein. Point mutations in the conserved region (CR3 - the

CC kinase domain) of c-raf-1 protein is indicative of increased risk of

CC developing cancer (particularly lung adenocarcinoma) and determining

CC the appropriate course of treatment.

XX Sequence 648 AA;

XX Query Match 100.0%; Score 3413; DB 20; Length 648;

XX Best Local Similarity 100.0%; Pred. No. 1.le-298;

XX Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHQCAWKTTSNGFGKDAVDFGSSCISPTIVQOFGYQRRASDGLTDPSTNTIRV 60

DB 1 MEHQCAWKTTSNGFGKDAVDFGSSCISPTIVQOFGYQRRASDGLTDPSTNTIRV 60

QY 61 FLPNKQRTVNVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHHEKCKKARLDNNTDAAS 120

DB 61 FLPNKQRTVNVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHHEKCKKARLDNNTDAAS 120

QY 121 LIGBELOVDFLDHVPFLTHNFARKFTFLKAFCDICQKFLNGFRQCOTCGYKFHEHCSTKV 180

DB 121 LIGBELOVDFLDHVPFLTHNFARKFTFLKAFCDICQKFLNGFRQCOTCGYKFHEHCSTKV 180

QY 181 PTMCVDRSNIRQLLFPNSTIGDSGVPALPSLTHRRMRESVSRMPVSSQHRYSSTPHAFTE 240

DB 181 PTMCVDRSNIRQLLFPNSTIGDSGVPALPSLTHRRMRESVSRMPVSSQHRYSSTPHAFTE 240

QY 241 NTSSPSSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSPPNNL 300

DB 241 NTSSPSSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSPPNNL 300

QY 301 SPTGNSQPTVPVPAQRERAPVSGTQEKNIIRPRGORDSSYWEIEASEVMLSTRIGSGSF 360

DB 301 SPTGNSQPTVPVPAQRERAPVSGTQEKNIIRPRGORDSSYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNILLFMGYMTKONLAIV 420

DB 361 GTVYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNILLFMGYMTKONLAIV 420

QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480

DB 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480

QY 481 TVKIGDFGLATVKSRSWGSQQVEQPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIYLYE 540

DB 481 TVKIGDFGLATVKSRSWGSQQVEQPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIYLYE 540

QY 541 LMTGELPYSHINNROQIIFWVGRCYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

DB 541 LMTGELPYSHINNROQIIFWVGRCYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 7

AAW30664

ID AAW30664 standard; Protein; 648 AA.

XX AAW30664;

XX 08-FEB-2001 (first entry)

XX Human OREF2465 polypeptide sequence SEQ ID NO:4930.

XX Human; open reading frame; OREF; detection; cytostatic; hepatotropic;

XX vulnary; antiproliferative; antiparkinsonian; neurotropic; neuroprotective;

XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;

XX hypotensive; dermatological; immunosuppressive; antiinflammatory;

XX antiviral; antibacterial; antifungal; antirheumatic; antithyroid;

XX antianaemic; gene therapy; cancer; proliferative disorder; hypertension;

XX neurodegenerative disorder; osteoarthritis; graft vs host disease;

XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
XX Homo sapiens.
XX WO200058473-A2.
XX PD 05-OCT-2000.
XX PF 31-MAR-2000; 2000WO-US08621.
XX PR 31-MAR-1999; 99US-0127607.
XX PR 02-APR-1999; 99US-0127636.
XX PR 05-APR-1999; 99US-0127728.
XX PR 30-MAR-2000; 2000US-0540763.
XX
XX (CURA-) CURAGEN CORP.
XX PA
XX PI Shinkets RA, Leach M;
XX DR WPI; 2000-602362/57.
XX DR N-PSDB; AAC76910.
XX
XX Novel nucleic acids and peptides derived from open reading frame x,
XX PT useful for treating e.g. cancers, proliferative disorders,
XX PT neurodegenerative disorders and cardiovascular disease -
XX PS
XX Claim 11; Page 4106-4107; 5507pp; English.
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
XX CC antiparasitic; antiparkinsonian; nootropic; neuroprotective;
XX CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
XX CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
XX CC antidiabetic; hypotensive; dermatological; immunosuppressive;
XX CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
XX CC antithyroid; and antianemic. The sequences can be used for determining
XX CC the presence of or predisposition to, or preventing or treating
XX CC pathological conditions associated with an ORFX-associated disorder. The
XX CC nucleic acids can be used to express ORFX proteins in gene therapy
XX CC vectors. The proteins and nucleic acids may be used to treat cancers,
XX CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
XX CC graft vs host disease, cardiovascular disease, diabetes mellitus,
XX CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
XX CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
XX CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
XX CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
XX CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
XX CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 21; Length 648;
Best Local Similarity 100.0%; Pred. NO. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTQGAWKTSINGFGKDAVDFGSSCSISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60
DB 1 MEHTQGAWKTSINGFGKDAVDFGSSCSISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60

QY 61 FLPNKQRTVVNRNGMSLHDLCKALKVRLGQIPECCAVFRLLEHKGKKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNRNGMSLHDLCKALKVRLGQIPECCAVFRLLEHKGKKARLDWNTDAAS 120

QY 121 LIGELQVDFLDHVPLTHNFARTFLKAFCDICQKFLNGRCOTCGYKFFHEHGSTKV 180
DB 121 LIGELQVDFLDHVPLTHNFARTFLKAFCDICQKFLNGRCOTCGYKFFHEHGSTKV 180

QY 181 PTMCDVMSNIRQLLLFPNSTIGDVGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTE 240

DB 181 PTMCDVMSNIRQLLLFPNSTIGDVGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTE 240
QY 241 NTSSPSSEGLSQRRORSTSTPNVHMVSTTLPVDSRWIEDAIRSHSESASPSALSSPNL 300
DB 241 NTSSPSSEGLSQRRORSTSTPNVHMVSTTLPVDSRWIEDAIRSHSESASPSALSSPNL 300
QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNNKIRPRGQDSYYWEIPEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNNKIRPRGQDSYYWEIPEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGKWHGDVAVKILKVVDDPTPQFOAFRNEVAVLKRTHRVNLLFPGYTKDNLAIV 420
DB 361 GTVYKKGKWHGDVAVKILKVVDDPTPQFOAFRNEVAVLKRTHRVNLLFPGYTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDTARQTAQGMIDLHAKNIHHRDKNNIFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQFQIDTARQTAQGMIDLHAKNIHHRDKNNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWSGQQVEQPTGSLVMAPEVIRMQDNNPFQSDVSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRWSGQQVEQPTGSLVMAPEVIRMQDNNPFQSDVSYGIVLYE 540
QY 541 LMTGELPYSHINRDQIIFMVGRGYASPDLSKLYKNCPRAMKRLVADCKVKKEERPLFP 600
DB 541 LMTGELPYSHINRDQIIFMVGRGYASPDLSKLYKNCPRAMKRLVADCKVKKEERPLFP 600
QY 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
DB 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648

RESULT 8
AAB08773
ID AAB08773 standard; protein; 648 AA.
XX
AC AAB08773;
XX DT 02-JAN-2001 (first entry)
XX DE Amino acid sequence of a human Raf-1 protein.
XX KW Intracellular signal transduction protein; antigen;
XX KW Systemic Lupus Erythematosus; inner ear; Raf-1.
XX OS Homo sapiens.
XX PN WO200050455-A2.
XX PD 31-AUG-2000.
XX PF 25-FEB-2000; 2000WO-US04770.
XX PR 25-FEB-1999; 99US-0121547.
XX PA (TAI/J) TAI J Y.
XX PI Yoo TJ;
XX WPI; 2000-572070/53.
XX
XX New 28 kDa antigen of the intracellular signal transduction protein,
XX PT useful for Systemic Lupus Erythematosus diagnosis, monitoring and
XX PT treatment -
XX
XX Example 4; Page 17-19; 36pp; English.
XX
XX The present sequence represents a human Raf-1 protein. The Raf-1
XX CC protein is homologous to an antigen of the intracellular signal
XX CC transduction protein. The antigen is reactive with antibodies from
XX CC patients with Systemic Lupus Erythematosus. The 28 kDa antigen is
XX CC present in the membranous fraction of the inner ear. The 28 kDa
XX CC antigen is useful for detecting Systemic Lupus Erythematosus in

CC animals, especially humans. The antigen is also useful for
CC immunotherapeutic treatment of Systemic Lupus Erythematosus.

XX
SQ Sequence 648 AA;

```
Query Match      100.0%; Score 3413; DB 21; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIOGAWKTSINGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIOGAWKTSINGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60

QY 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120
Db 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120

QY 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFCOTCGYKFHEHCSTKV 180
Db 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFCOTCGYKFHEHCSTKV 180

QY 181 PTMCVDWNSIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSPTHAFTF 240
Db 181 PTMCVDWNSIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSPTHAFTF 240

QY 241 NTSSPSSEGSLSQRRSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSSEGSLSQRRSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300

QY 301 SPTGWSQKTPVPAQERAPVSGTQEKNIKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQERAPVSGTQEKNIKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKKGWGDVAVKILKVVDTPPEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420
Db 361 GTVYKKGWGDVAVKILKVVDTPPEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420

QY 421 TQWCGSSLYKHLHVOETKFOQLIDTARQAGMDYLHAKNIHHRDKMKNITFLHREGL 480
Db 421 TQWCGSSLYKHLHVOETKFOQLIDTARQAGMDYLHAKNIHHRDKMKNITFLHREGL 480

QY 481 TVKIGDFGLATVKSRSWSQSQVEQPTGSLVMAPEVIRMQDNNPFSQSDYVSGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWSQSQVEQPTGSLVMAPEVIRMQDNNPFSQSDYVSGIVLYE 540

QY 541 LMTGELPYSHINNRQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 600
Db 541 LMTGELPYSHINNRQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
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RESULT 9
AAY94501

XX AAY94501 standard; Protein; 648 AA.

AC AAY94501;

XX 20-SEP-2000 (first entry)

XX Human c-ras protein.

KW Antisense; E-selectin; TNF alpha; cell adhesion; human;
KW tumour necrosis factor alpha; phosphorothioate; methoxyethoxy;
KW sepsis; rheumatoid arthritis; inflammatory; immune disease;
KW inflammatory bowel disease; allergic contact dermatitis; psoriasis;
KW diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
KW immunosuppressive; antipsoriatic; antidiabetic; antithyroid;
KW cytostatic; dermatological; antiallergic; Ha-ras; c-ras;
KW c-Jun N-terminal kinase; JNK; ds.

XX

OS Homo sapiens.
XX WO200034303-A1.

XX 15-JUN-2000.

XX 08-DEC-1999; 99WO-US28965.

XX 10-DEC-1998; 98US-0209668.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Xu XS;

XX WPI; 2000-423367/36.

XX N-PSDB; AAA48654.

XX Modulating cell adhesion molecule expression for treating immune or
XX inflammatory diseases involves treating cell with specific inhibitor of
XX Tumour Necrosis Factor alpha signalling molecule.

XX Disclosure; Page 83-85; 100pp; English.

CC A novel method for modulating cell adhesion molecule expression
CC involves antisense inhibition of a tumour necrosis factor (TNF) alpha
CC signalling molecule. In the method TNF alpha signalling molecules
CC Ha-ras, c-ras and c-Jun N-terminal kinase (JNK)2 were inhibited by
CC antisense oligonucleotides. In addition an antisense oligonucleotide
CC to the cell adhesion molecule E-selectin was also examined. The
CC present sequence is human c-ras protein. The DNA encoding this sequence
CC was used to generate the c-ras antisense oligonucleotide. The antisense
CC oligonucleotides used in the method contained modifications,
CC namely phosphorothioate linkages and 2'methoxyethoxy bases. Some
CC C residues also had a 5'methyl modification. Inhibitors of the TNF
CC alpha signalling molecules have antibacterial, immunosuppressive,
CC antiproliferative, antidiabetic, antithyroid, cytostatic, dermatological,
CC anti-allergic and anti-inflammatory activity. The antisense inhibitors
CC may be useful for the treatment of sepsis, rheumatoid arthritis,
CC inflammatory, immune disease, inflammatory bowel disease, allergic
CC contact dermatitis, psoriasis, diabetes, Grave's disease, allograft
CC rejection and cancer.

XX Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 21; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MEHIOGAWKTSINGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIOGAWKTSINGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60

QY 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120
Db 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120

QY 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFCOTCGYKFHEHCSTKV 180
Db 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFCOTCGYKFHEHCSTKV 180

QY 181 PTMCVDWNSIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSPTHAFTF 240
Db 181 PTMCVDWNSIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSPTHAFTF 240

QY 241 NTSSPSSEGSLSQRRSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSSEGSLSQRRSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300

QY 301 SPTGWSQKTPVPAQERAPVSGTQEKNIKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQERAPVSGTQEKNIKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKKGWGDVAVKILKVVDTPPEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420
```

Db 361 GTVYKGWHDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILLEFGYMTKDLAIY 420
Qy 421 TQWCEGSSLYKHLHVOETKFOFQIDIAQTQAGMDYLHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVOETKFOFQIDIAQTQAGMDYLHAKNIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRWGSQOVBQPTGSLVWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWGSQOVBQPTGSLVWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Qy 541 LMTGELPYSHINRDQIIFWVGSGYASDLSKLYKNCPRAMKRLVADCVKKVEERPLFP 600
Db 541 LMTGELPYSHINRDQIIFWVGSGYASDLSKLYKNCPRAMKRLVADCVKKVEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
RESULT 10
AAB70295
ID AAB70295 standard; Protein; 648 AA.
XX AAB70295;
DT 10-MAY-2001 (first entry)
XX Human c-Raf protein.
DE Raf; ras; vector; tumour; arthritis; retinopathy; angioplasty.
KW Homo sapiens.
OS WO200112210-A1.
PN 22-FEB-2001.
PD 11-AUG-2000; 2000WO-US21842.
PF 13-AUG-1999; 99US-0148924.
PR 05-JUL-2000; 2000US-0215951.
XX (SCRI) SCRIPPS RES INST.
PI Hood J, Elliceiri B, Cheresh DA;
XX WPI; 2001-202826/20.
XX Composition for modulating angiogenesis and treating rheumatoid
PT arthritis and restenosis comprises Raf protein or viral or non-viral
PT gene transfer vector containing nucleic acid encoding for Raf or Ras
PT protein -
XX Disclosure; Fig 8; 102pp; English.
XX The present invention relates to a composition with a
CC Raf protein or a viral or non-viral gene transfer vector containing
CC a nucleic acid encoding for a Raf or Ras protein. The Raf
CC protein optionally has kinase activity and the Ras protein has
CC angiogenesis modulating activity. The invention is useful for
CC modulating angiogenesis in a tissue which has poor or abnormal
CC circulation, in a tissue which is a solid tumor or solid tumour
CC metastasis, in an inflamed tissue associated with arthritis or
CC rheumatoid arthritis, in a retinal tissue associated with retinopathy,
CC diabetic retinopathy or macular degeneration, or in a tissue which is
CC at the site of coronary angioplasty associated with restenosis.
XX
XX Sequence 648 AA;
Query Match 100.0%; Score 3413; DB 22; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEHIQGAWKTISNGFGFKDAVDFDSSCISPTIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
Db 1 MEHIQGAWKTISNGFGFKDAVDFDSSCISPTIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
Qy 61 FLPNKQRTVVNVRNGMSLHDCIMKALKVKGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMSLHDCIMKALKVKGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
Qy 121 LIGELQVDFLDHVPVLTTHNFARKTFKLAFCDICQKFLNGFRQCQCGYKFHCHCSTKV 180
Db 121 LIGELQVDFLDHVPVLTTHNFARKTFKLAFCDICQKFLNGFRQCQCGYKFHCHCSTKV 180
Qy 181 PTMCVDWNSINRQLLFPNSTIGDGVPPALPSLTWRRMRESVSRMPVSSQHRYSPTPHAF 240
Db 181 PTMCVDWNSINRQLLFPNSTIGDGVPPALPSLTWRRMRESVSRMPVSSQHRYSPTPHAF 240
Qy 241 NTSSPSSSEGLSQRORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSSPNNL 300
Db 241 NTSSPSSSEGLSQRORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSSPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
Qy 361 GTVYKGWHDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILLEFGYMTKDLAIY 420
Db 361 GTVYKGWHDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILLEFGYMTKDLAIY 420
Qy 421 TQWCEGSSLYKHLHVOETKFOFQIDIAQTQAGMDYLHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVOETKFOFQIDIAQTQAGMDYLHAKNIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRWGSQOVBQPTGSLVWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWGSQOVBQPTGSLVWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Qy 541 LMTGELPYSHINRDQIIFWVGSGYASDLSKLYKNCPRAMKRLVADCVKKVEERPLFP 600
Db 541 LMTGELPYSHINRDQIIFWVGSGYASDLSKLYKNCPRAMKRLVADCVKKVEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
RESULT 11
AAG67440
ID AAG67440 standard; Protein; 648 AA.
XX AAG67440;
AC AAG67440;
DT 26-NOV-2001 (first entry)
XX Amino acid sequence of a human polypeptide.
DE Human; protein kinase; protein phosphatase; signal transduction;
KW intracellular signalling pathway.
XX Homo sapiens.
XX WO200109345-A1.
XX 08-FEB-2001.
PD 28-JUL-2000; 2000WO-JP05060.
PF 29-JUL-1999; 99JP-0248036.
PR 18-OCT-1999; 99US-0159590.
PR 11-JAN-2000; 2000JP-0118776.
PR 17-FEB-2000; 2000US-0183322.
PR 02-MAY-2000; 2000JP-0183767.
XX

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
Senoo C, Nezu J;

WPI: 2001-564736/63.

New genes encoding protein kinase and protein phosphatase, useful for
identifying modulators which can be used to treat human or animal
disorders associated with the expression or function of these enzymes -
Example 4; Page 213-218; 336pp; Japanese.

The specification describes human protein kinase/protein phosphatases.
The polypeptides are expected to participate in signal transduction
in cells. The kinase phosphatases are connected with intracellular
signalling pathways. Antisense oligonucleotides and compounds
identified by screening (agonists or antagonists) can be used to
treat human or animal disorders associated with the expression
or function of the protein. In addition, the polypeptides may be used
as target molecules for drug development. The present sequence
represents a polypeptide, used in the course of the invention.

Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 22; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.le-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIOGAWKTSNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIOGAWKTSNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLPNKQRTVVNVNRGMSLHDCMLKALKVRGLQPECCAVFLLHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNVNRGMSLHDCMLKALKVRGLQPECCAVFLLHEHKGKARLDWNTDAAS 120
QY 121 LIGEELOVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFRCTCGYKFEHCSTKV 180
DB 121 LIGEELOVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFRCTCGYKFEHCSTKV 180
QY 181 PTMCDVNSIRQLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSOHRYSTPHFTTF 240
DB 181 PTMCDVNSIRQLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSOHRYSTPHFTTF 240
QY 241 NTSSPSSGSLSQORSTSTPNVHMVSTTLVPDSRMIEDAIRSHSESASPSALSSSPNNL 300
DB 241 NTSSPSSGSLSQORSTSTPNVHMVSTTLVPDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIPRGQDSSYYWETEASEVLMSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIPRGQDSSYYWETEASEVLMSTRIGSGSF 360
QY 361 GTVYKGRWHGDVAVKILKVVDPTEQFOAFNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
DB 361 GTVYKGRWHGDVAVKILKVVDPTEQFOAFNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
QY 421 TQWCEGSLYKHLHVQETKQFOMQLIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
DB 421 TQWCEGSLYKHLHVQETKQFOMQLIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
QY 481 TVKIGDGLAVYKSRWSGQVEQPTGSLVLMAPDEVIRMQDNPFPQSQSVYGYVLYE 540
DB 481 TVKIGDGLAVYKSRWSGQVEQPTGSLVLMAPDEVIRMQDNPFPQSQSVYGYVLYE 540
QY 541 LMTGELPYSHINNRDQIIFWVGRCYASPDLSKYNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRDQIIFWVGRCYASPDLSKYNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPYF 648
DB 601 QILSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPYF 648

RESULT 12

RAG67619

ID AAG67619 standard; Protein; 648 AA.

XX AAG67619;

XX AC

XX AC

XX DT

XX DT

XX DE

XX DE

XX KW

XX KW

XX OS

XX OS

XX PN

XX PN

XX PD

XX PD

XX PF

XX PF

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

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XX PR

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XX PR

XX PR

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XX PR

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XX PR

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XX PR

Db 181 PTMCVDMSNRQLLFPNSIGSGVPALPSTLTMRRRESVSRMPVSSQHRSTPHAFTE 240
Qy 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
Qy 301 SPTGWSQKTPVPAQRERAPVSGTQEKNKIRPRGDRSSYYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTQEKNKIRPRGDRSSYYWEIEASEVYMLSTRIGSGSF 360
Qy 361 GTVYKGWHDGAVKILKVVDPTEQFOAFRNEAVLKRTRHVNILLFNGYTKDNLAIY 420
Db 361 GTVYKGWHDGAVKILKVVDPTEQFOAFRNEAVLKRTRHVNILLFNGYTKDNLAIY 420
Qy 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQVQEQPTGCVLWMAPEVIRMODNPFQSDVYSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQVQEQPTGCVLWMAPEVIRMODNPFQSDVYSYGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFWVGGRYASPDLSKLYKNCPCAMKRLVADCVKKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFWVGGRYASPDLSKLYKNCPCAMKRLVADCVKKKEERPLFP 600
Qy 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 13
ABB76179
ID ABB76179 standard; Protein: 648 AA.
AC ABB76179;
XX
DT 22-JUL-2002 (first entry)
DE Human protein kinase C-Raf.
KW C-Raf; protein kinase; human; antitumour; antidiabetic;
KW antinflammatory; vasotropic; vulnerary; antithrombotic;
KW neuroprotective; nootropic; cerebroprotective; antipsoriatic;
KW antiarthritic; signal transduction; gene therapy.
XX
OS Homo sapiens.
XX WO200226246-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-EP11282.
XX
PR 29-SEP-2000; 2000EP-0121490.
XX
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI Hatzopoulos A, Hautmann M, Herbst M, Geishauser A, Schoch J;
XX WPI; 2002-402033/43.
DR N-PSDB; ABL57050.
XX
PT Composition for treating or preventing pathological conditions in which
PT endothelial cells are involved or affected e.g. diabetes, inflammation,
PT psoriasis, has Raf protein, polynucleotide, or modulators of the
PT protein -
XX
PS Claim 1; Page 62-64; 64pp; English.
XX
CC The present sequence is the protein sequence of human C-Raf, a
CC protein kinase involved in signal transduction cascades. The

CC invention provides pharmaceutical compositions (PCs) comprising
CC a polynucleotide encoding a Raf protein, especially A-Raf, B-Raf
CC or C-Raf, in particular B-Raf, a vector comprising and capable of
CC expressing the polynucleotide, host cells genetically engineered
CC with the polynucleotide or vector, a polypeptide encoded by the
CC polynucleotide, agonists or antagonists of the polypeptide and the
CC methods of identifying them, and diagnostic compositions. The PCs
CC are used to prevent or treat a condition in which endothelial
CC cells are involved or affected, by inhibiting or promoting
CC angiogenesis, modulating the permeability of the blood-brain
CC barrier, or by blocking or enhancing cell migration during
CC angiogenesis or tissue remodelling. The PCs are useful for treating
CC or preventing tumours, diabetic retinopathy, chronic inflammatory
CC disease, restenosis, cardiomyopathy, inflammation, atherosclerosis,
CC stroke or myocardial infarction, for promoting wound healing,
CC enhancing circulation, inhibiting tumour development especially
CC metastasis, for treating pathophysiological conditions or injury of
CC the vascular wall, Alzheimer's disease, and for preventing
CC coagulation or fibrin deposition in the vessels (all claimed). A
CC claimed diagnostic composition comprising a Raf polynucleotide,
CC vector, host cell, polypeptide or antibody, is useful for diagnosing
CC a pathological condition or a susceptibility to a pathological
CC condition in a subject, by determining the expression level of Raf
CC in a sample.
XX
SQ Sequence 648 AA;
Query Match 100.0%; Score 3413; DB 23; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-398;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEHIOGANKTISNGFGFKDAVDFGSSCISPIVQOFGYQRRASDDGKLTDPKTSNIRV 60
Db 1 MEHIOGANKTISNGFGFKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKTSNIRV 60
Qy 61 FLPNKQRTVVNVNRGMSLHDCMLKALKVRLQPECCAVFLLHGHKGLKARLDNNTAAS 120
Db 61 FLPNKQRTVVNVNRGMSLHDCMLKALKVRLQPECCAVFLLHGHKGLKARLDNNTAAS 120
Qy 121 LIGELQVDFLDHVPLTTHNFARKTFLKAFDCICQKFLNGFCQTCGYKFHEHCSTKV 180
Db 121 LIGELQVDFLDHVPLTTHNFARKTFLKAFDCICQKFLNGFCQTCGYKFHEHCSTKV 180
Qy 181 PTMCVDMSNRQLLFPNSTIGDGVLPALPSLTMRRRESVSRMPVSSQHRSTPHAFTE 240
Db 181 PTMCVDMSNRQLLFPNSTIGDGVLPALPSLTMRRRESVSRMPVSSQHRSTPHAFTE 240
Qy 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
Qy 301 SPTGWSQKTPVPAQRERAPVSGTQEKNKIRPRGDRSSYYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTQEKNKIRPRGDRSSYYWEIEASEVYMLSTRIGSGSF 360
Qy 361 GTVYKGWHDGAVKILKVVDPTEQFOAFRNEAVLKRTRHVNILLFNGYTKDNLAIY 420
Db 361 GTVYKGWHDGAVKILKVVDPTEQFOAFRNEAVLKRTRHVNILLFNGYTKDNLAIY 420
Qy 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQVQEQPTGCVLWMAPEVIRMODNPFQSDVYSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQVQEQPTGCVLWMAPEVIRMODNPFQSDVYSYGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFWVGGRYASPDLSKLYKNCPCAMKRLVADCVKKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFWVGGRYASPDLSKLYKNCPCAMKRLVADCVKKKEERPLFP 600
Qy 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 14
AAG80183

ID AAG80183 standard; Protein; 648 AA.

XX AAG80183;

21-JAN-2002 (first entry)

Human c-raf-1 protein.

Oncogene; c-raf-1; human; MEK1; MEK kinase; raf-binding; cytostatic;
mitogen activated and extracellular stimuli regulated kinase;
gene therapy; NF-kB suppression; tumour cell proliferation;
NF-kB-mediated signal cascade.

OS Homo sapiens.

PN WO200179501-A2.

PD 25-OCT-2001.

XX 17-APR-2001; 2001WO-DE01518.

PR 14-APR-2000; 2000DE-1020138.

XX (RAPP/) RAPP U R.
PA (WIRT/) WIRTH T.

XX Rapp UR, Wirth T;

XX WPI: 2002-017617/02.

DR N-PSDB; RAI68698.

XX New nucleic acid encoding partial raf sequence, useful for identifying
PT compounds that block binding of raf to its activating kinase as
PT potential anticancer agents

XX Disclosure; Fig 10b-f; 66pp; German.

XX This invention describes a novel nucleic acid (I) that: (i) encodes at
CC least one raf partial sequence containing a MEK1 (mitogen activated and
CC extracellular stimuli regulated (MEK) kinase) binding site; (ii) encodes
CC at least one partial sequence of MEK1 containing a raf binding site;
CC (iii) is a silent mutation of (i) or (ii); or (iv) hybridizes to
CC (i)-(iii). The products of the invention have cytostatic activity and can
CC be used for gene therapy. The products also suppress NF-kB activation
CC resulting in inhibition of tumour cell proliferation or transformation.
CC (I), or proteins/peptides encoded by them, are useful for identifying
CC compounds that block binding of raf to MEK1. These compounds, optionally
CC where expressed from gene therapy vectors, are useful in human or
CC veterinary medicine for treatment of tumors. Antisense sequences, or
CC ribozymes, that bind to (I) are used to inhibit MEK1 activation. Also
CC nucleic acid (I') encoding at least a part of raf (or its silent
CC mutations or hybridizing sequences) is used to examine interaction of
CC encoded proteins with activation of the NF-kB-mediated signal cascade and
CC to screen for inhibitors of cell transformation by raf-mediated
CC activation of NF-kB. This sequence represents the human c-raf-1 oncogene
CC described in the method of the invention.

XX Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 23; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQGAWKTIISNGFGKDAVDFGSSCISPTIQQFGYQRRASDDKGLTDPKTSNTIRV 60
DB 1 MEHIQGAWKTIISNGFGKDAVDFGSSCISPTIQQFGYQRRASDDKGLTDPKTSNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDKLMKALVGRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120

Db 61 FLPNKQRTVVNVRNGMSLHDKLMKALVGRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120
QY 121 LIGEELOVDLHDVPLTTHNFARKYFLKLAFCDICOKELLNGFCOTCGYKPFHEHCSTKV 180
Db 121 LIGEELOVDLHDVPLTTHNFARKYFLKLAFCDICOKELLNGFCOTCGYKPFHEHCSTKV 180
QY 181 PTMCDWMSNIROLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSYTPHATF 240
Db 181 PTMCDWMSNIROLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSYTPHATF 240
QY 241 NTSSPSSGSLSORQRSTSTPNVHVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
Db 241 NTSSPSSGSLSORQRSTSTPNVHVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
QY 301 SPTGWSQKTPVPAQREAPVSGTQKKNIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQREAPVSGTQKKNIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKGKWHGDVAVKILKVVDTPPEQFAFRNEVAVLRKTRHVNILLFMYGMYTKDNLAIV 420
Db 361 GTVYKGKWHGDVAVKILKVVDTPPEQFAFRNEVAVLRKTRHVNILLFMYGMYTKDNLAIV 420
QY 421 TWCCEGSSLYKHLHVQETKFMFLIDTARQTAQGM DYLHAKNIITHRDMKSNIFLHGL 480
Db 421 TWCCEGSSLYKHLHVQETKFMFLIDTARQTAQGM DYLHAKNIITHRDMKSNIFLHGL 480
QY 481 TVKIGDFGLATVKSRSWSSQOQVEPTGSLVWNAPEVIRMQDNNPFSQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVKSRSWSSQOQVEPTGSLVWNAPEVIRMQDNNPFSQSDVYSYGVLYE 540
QY 541 LMTGELPYSHINNROQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNROQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 15
AAB70297

ID AAB70297 standard; Protein; 668 AA.

XX AAB70297;

DT 10-MAY-2001 (first entry)

XX Raf-caax fusion protein.

DE Raf; ras; vector; tumour; arthritis; retinopathy; angioplasty.

XX Homo sapiens.

PN WO200112210-A1.

XX 22-FEB-2001.

PF 11-AUG-2000; 2000WO-US21842.

PR 13-AUG-1999; 99US-0148924.

PR 05-JUL-2000; 2000US-0215951.

XX (SCRI) SCRIPPS RES INST.

XX Hood J, Elliceiri B, Cheresh DA;

XX WPI: 2001-202826/20.

XX Composition for modulating angiogenesis and treating rheumatoid
PT arthritis and restenosis comprises Raf protein or viral or non-viral
PT gene transfer vector containing nucleic acid encoding for Raf or Ras
PT protein

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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:37:02 ; Search time 26 Seconds
(without alignments)
1033.718 Million cell updates/sec

Title: US-09-637-302C-2

Perfect score: 3413

Sequence: 1 MEHQGAWKTSNGFGKDA.....AHTEDINACTLTTSPLPVF 648

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3413	100.0	648	1 KRAF_HUMAN	P04049 homo sapien
2	3349	98.1	648	1 KRAF_RAT	P11345 rattus norv
3	3249.5	95.2	647	1 KMIL_CHICK	P05625 gallus gall
4	2885	84.5	638	1 KRAF_XENLA	P09560 xenopus lae
5	1893.5	55.5	606	1 KRAA_FIG	O19004 sus scrofa
6	1891.5	55.4	604	1 KRAA_RAT	P14056 rattus norv
7	1890.5	55.4	604	1 KRAA_MOUSE	P04627 mus musculu
8	1889.5	55.4	606	1 KRAA_HUMAN	P10398 homo sapien
9	1888.5	55.3	380	1 KMIL_AVTMH	P00531 avian retro
10	1825	53.5	765	1 KRAF_HUMAN	P15056 homo sapien
11	1814	53.1	806	1 RMIL_CHICK	Q04982 gallus gall
12	1814	53.1	807	1 RMIL_COTJA	P34908 coturnix co
13	1654	48.5	323	1 KRAF_MSV36	P00532 murine sarc
14	1360	39.8	781	1 KRAF_DRONE	P11346 drosophila
15	1336	39.1	450	1 RMIL_AVEVR	P27966 avian rous-
16	1327.5	38.9	367	1 RMIL_AVTII	P10533 avian retro
17	1277	37.4	328	1 KRAF_MOUSE	P28028 mus musculu
18	1121.5	32.9	813	1 KRAF_CAEEL	Q07292 caenorhabdi
19	455.5	13.3	821	1 CTR1_ARATH	Q05609 arabidopsis
20	412.5	12.1	568	1 SRC_AVIS2	P14084 avian sarco
21	407	11.9	528	1 YES_AVISY	P00527 avian sarco
22	404	11.8	505	1 FRK_HUMAN	P2685 homo sapien
23	404	11.8	541	1 YES_CHICK	P09324 gallus gall
24	403	11.8	536	1 FYN_HUMAN	P06241 homo sapien
25	403	11.8	536	1 FYN_XENLA	P13406 xenopus lae
26	402	11.8	536	1 FYN_XIPHE	P27446 xiphophorus
27	401.5	11.8	505	1 SRK1_SPOLA	P42685 spongilla l
28	401	11.7	544	1 YES_XIPHE	P27447 xiphophorus
29	397	11.6	535	1 SRC_HUMAN	P12931 homo sapien
30	396	11.6	539	1 YES_CANFA	Q28923 canis famil
31	395	11.6	532	1 SRC_CHICK	P00523 gallus gall
32	395	11.6	543	1 YES_HUMAN	P07947 homo sapien
33	395	11.6	557	1 SRC_AVIS1	P14085 avian sarco

RESULT 1

ID	KRAF_HUMAN	STANDARD;	PRT;	648 AA.
AC	P04049;			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	01-NOV-1986 (Rel. 03, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.1.-)			
DE	(RAF-1) (C-RAF).			
GN	RAF1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86120351; PubMed=3003687;			
RA	Bonner T.I., Oppermann H., Seeburg P., Kerby S.B., Gunnell M.A.,			
RA	Young A.C., Rapp U.R.;			
RT	"The complete coding sequence of the human raf oncogene and the			
RT	corresponding structure of the c-raf-1 gene.";			
RL	Nucleic Acids Res. 14:1009-1015(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pancreas;			
RA	Strausberg R.;			
RN	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	PHOSPHORYLATION.			
RX	MEDLINE=99039505; PubMed=9823899;			
RA	King A.J., Sun H., Diaz B., Barnard D., Miao W., Bagrodia S.,			
RA	Marshall M.S.;			
RT	"The protein kinase Pak3 positively regulates Raf-1 activity through			
RT	phosphorylation of serine 338.";			
RL	Nature 396:180-183(1998).			
RN	[4]			
RP	ERRATUM.			
RA	King A.J., Sun H., Diaz B., Barnard D., Miao W., Bagrodia S.,			
RA	Marshall M.S.;			
RL	Nature 406:439-439(2000).			
RN	[5]			
RX	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 51-131.			
RP	MEDLINE=95312074; PubMed=7791872;			
RA	Nassar N., Horn G., Herrmann C., Scherer A., McCormick F.,			
RA	Wittinghofer A.;			
RT	"The 2.2 A crystal structure of the Ras-binding domain of the			
RT	serine/threonine kinase c-Raf1 in complex with Rap1A and a GTP			
RL	analogue.";			
RL	Nature 375:554-560(1995).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 56-131.			
RX	MEDLINE=96313130; PubMed=8756332;			
RA	Nassar N., Horn G., Herrmann C., Block C., Janknecht R.,			
RA	Wittinghofer A.;			
RT	"Ras/Rap effector specificity determined by charge reversal.";			
RL	Nat. Struct. Biol. 3:723-729(1996).			

P15054 avian sarco
P05480 mus musculu
O04736 mus musculu
P42689 spongilla l
P13116 xenopus lae
O9wud9 rattus norv
P13115 xenopus lae
P29320 homo sapien
P42683 gallus gall
P39688 mus musculu
Q02977 gallus gall
P10936 xenopus lae

ALIGNMENTS

[7]
 RN STRUCTURE BY NMR OF 55-132.
 RX MEDLINE=95284022; PubMed=7766599;
 RA Emerson S.D., Madison V.S., Palermo R.E., Waugh D.S., Scheffler J.E.,
 RA Tsao K.L., Kiefer S.E., Liu S.P., Fry D.C.;
 RT "Solution structure of the Ras-binding domain of c-Raf-1 and
 RT identification of its Ras interaction surface.";
 RL Biochemistry 34:6911-6918(1995).
 [8]
 RN STRUCTURE BY NMR OF 136-187.
 RX MEDLINE=96323218; PubMed=8710867;
 RA Mott H.R., Carpenter J.W., Zhong S., Ghosh S., Bell R.M.,
 RA Campbell S.L.;
 RT "The solution structure of the Raf-1 cysteine-rich domain: a novel
 RT ras and phospholipid binding site.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8312-8317(1996).
 CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM
 CC THE CELL MEMBRANE TO THE NUCLEUS. PART OF THE RAS-DEPENDENT
 CC SIGNALING PATHWAY FROM RECEPTORS TO THE NUCLEUS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; X03484; CAA27204.1; -;
 DR EMBL; BC018119; AAH18119.1; -;
 DR PIR; A00637; TVHUF6.
 DR PDB; 1FAQ; 27-JAN-97.
 DR PDB; 1FAR; 27-JAN-97.
 DR PDB; 1FEA; 20-JUN-96.
 DR PDB; 1GUA; 11-JAN-97.
 DR Genem; HGNC:9829; RAF1.
 DR MIM; 164760; -;
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003116; RBD.
 DR InterPro; IPR004040; STY_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00130; DAG_PE-bind; 1.
 DR Pfam; PF02196; RBD; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00109; Cl; 1.
 DR SMART; SM00455; RBD; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM.1; 1.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM.2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
 KW ATP-binding; Phorbol-ester binding; Phosphorylation; 3D-structure.
 FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 349 609 PROTEIN KINASE.
 FT NP_BIND 355 363 ATP (BY SIMILARITY).
 FT BINDING 375 375 ATP (BY SIMILARITY).
 FT ACT_SITE 468 468 BY SIMILARITY.
 FT MOD_RES 338 338 PHOSPHORYLATION (BY PAK2 AND PAK3).
 SQ SEQUENCE 648 AA; EF821B5349711BC3 CRC64;
 Query Match 100.0%; Score 3413; DB 1; Length 648;
 Best Local Similarity 100.0%; Pred. No. 3.6e-223;
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQCAWKTSINGFGFKDAVDFGSSCISPIIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
 DB 1 MEHIQCAWKTSINGFGFKDAVDFGSSCISPIIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
 QY 61 FLPNKQRTVNVNRNGMSLHDCMLKALKVGRLOPCCCAVRLHHEHKGKARLDWNTDAAS 120
 DB 61 FLPNKQRTVNVNRNGMSLHDCMLKALKVGRLOPCCCAVRLHHEHKGKARLDWNTDAAS 120
 QY 121 LIGEELOVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGLNGFCQTCGKFEHCSTKV 180
 DB 121 LIGEELOVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGLNGFCQTCGKFEHCSTKV 180
 QY 181 PTMCVDNSINRQQLLLFPNSTIGDSVPALPSLTWRRMRRESVSRMPVSSQHRYSPTPHTFF 240
 DB 181 PTMCVDNSINRQQLLLFPNSTIGDSVPALPSLTWRRMRRESVSRMPVSSQHRYSPTPHTFF 240
 QY 241 NTSSPSSGSLSQQRSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
 DB 241 NTSSPSSGSLSQQRSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
 QY 301 SPTGWSQPKTPVPAQRRAPVSGTQENKIRPQRDSSYYWEIEASEVMLSTRIGSGSF 360
 DB 301 SPTGWSQPKTPVPAQRRAPVSGTQENKIRPQRDSSYYWEIEASEVMLSTRIGSGSF 360
 QY 361 GTVYKGWHGDAVKILKVVDPTEQQAQFNEVAVLRKTHVNVILLFMGYMTKDNLAIV 420
 DB 361 GTVYKGWHGDAVKILKVVDPTEQQAQFNEVAVLRKTHVNVILLFMGYMTKDNLAIV 420
 QY 421 TQWCEGSSLYKHLHVQETKFMFQOLIDIARQAGMDYLHAKNIHHRDKSNINFLHEGL 480
 DB 421 TQWCEGSSLYKHLHVQETKFMFQOLIDIARQAGMDYLHAKNIHHRDKSNINFLHEGL 480
 QY 481 TVKIGDFGLATVKSRWSGQQVEQPTGSLVMAPEVIRMQDNNPFSQSDYSYGIYLYE 540
 DB 481 TVKIGDFGLATVKSRWSGQQVEQPTGSLVMAPEVIRMQDNNPFSQSDYSYGIYLYE 540
 QY 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRVADCVKVKKEERPLFP 600
 DB 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRVADCVKVKKEERPLFP 600
 QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPYF 648
 DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPYF 648
 RESULT 2
 ID KRAF_RAT STANDARD; PRF; 648 AA.
 AC P11345;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)
 GN (RAF-1) (C-RAF).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87172791; PubMed=3550433;
 RA Ishikawa F., Takaku F., Nagao M., Sugimura T.;
 RT "Rat c-raf oncogene activation by a rearrangement that produces a
 RT fused protein.";
 RL Mol. Cell. Biol. 7:1226-1232(1987).
 RN [2]
 RP STRUCTURE BY NMR OF 51-131.
 RX MEDLINE=99134400; PubMed=9931261;
 RA Terada T., Ito Y., Shirouzu M., Tateno M., Hashimoto K., Kigawa T.,
 RA Ebisuzaki T., Takio K., Shibata T., Yokoyama S., Smith B.O.,
 RA Laue E.D., Cooper J.A.;
 RT "Nuclear magnetic resonance and molecular dynamics studies on the

interactions of the Ras-binding domain of Raf-1 with wild-type and mutant Ras proteins.;

J. Mol. Biol. 286:219-232(1999).

-|- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM THE CELL MEMBRANE TO THE NUCLEUS. PART OF THE RAS-DEPENDENT SIGNALING PATHWAY FROM RECEPTORS TO THE NUCLEUS.

-|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MIL/RAF SUBFAMILY.

-|- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.

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EMBL; M15427; AAA42001.1; ;
 PIR; A26126; TVTRF.
 PIR; B26126; TVTRF.
 PDB; 1RRB; 30-MAR-99.
 InterPro; IPR002219; DAG_PE-bind.
 InterPro; IPR000719; Euk_pkinase.
 InterPro; IPR003116; RBD.
 InterPro; IPR004040; STY_pkinase.
 InterPro; IPR002290; Ser_thr_pkinase.
 Pfam; PF00130; DAG_PE-bind; 1.
 Pfam; PF02196; RBD; 1.
 PRINTS; PR00008; DAGPEDOMAIN.
 ProDom; PD000001; Euk_pkinase; 1.
 SMART; SM00109; Cl; 1.
 SMART; SM00455; RBD; 1.
 SMART; SM00221; STYKc; 1.
 PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 Transferrase; Serine/threonine-protein kinase; Proto-oncogene; Zinc; ATP-binding; Phosphorylation; Phorbol-ester binding; 3D-structure.
 KW ATP-binding; Phosphorylation; Phorbol-ester AND DAG BINDING.
 FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.
 FT NP_BIND 349 509 PROTEIN KINASE.
 FT BINDING 355 363 ATP (BY SIMILARITY).
 FT ACT_SITE 375 375 ATP (BY SIMILARITY).
 FT MOD_RES 468 468 BY SIMILARITY.
 FT MOD_RES 499 499 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 648 AA; 72928 MW; 59AFB5975064193E CRC64;

Query Match 98.18; Score 3349; DB 1; Length 648;
 Best Local Similarity 98.3%; Pred. No. 7.6e-219;
 Matches 637; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 MEHTOGAWKTSNGFGKDAVFDGSSCISPTIVQFGYQRRASDGLKTOPSKTSNIRV 60
 DB 1 MEHTOGAWKTSNGFGKDAVFDGSSCISPTIVQFGYQRRASDGLKTOPSKTSNIRV 60
 QY 61 FLNPKQRTVNVNRGMSLHDCMLKALVRLQPCCAVFLHHEKCKKARLDWNTDAAS 120
 DB 61 FLNPKQRTVNVNRGMSLHDCMLKALVRLQPCCAVFLHHEKCKKARLDWNTDAAS 120
 QY 121 LIGELQVDFLDHVLTHNFARKTFLKLAFCDCQKFLNGFRQCOTGCKFHEHCSTKV 180
 DB 121 LIGELQVDFLDHVLTHNFARKTFLKLAFCDCQKFLNGFRQCOTGCKFHEHCSTKV 180
 QY 181 PTMCVDKSNIRQLLFNPNSTIGDSGVPALPSLTHRRMRRESVSRMPVSSQHYSTPHFTF 240
 DB 181 PTMCVDKSNIRQLLFNPNSTIGDSGVPALPSLTHRRMRRESVSRMPVSSQHYSTPHFTF 240
 QY 241 NTSSPSSEGSLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSSALSSPPNNL 300
 DB 241 NTSSPSSEGSLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSSALSSPPNNL 300

Db 241 NTSSPSSEGSLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSSALSSPPNNL 300
 QY 301 SPGTGWSQKTPVPAQERAPVSGTQKKNIRPGQDSSYYWIEASEVNLSTRIGSGSF 360
 Db 301 SPGTGWSQKTPVPAQERAPVSGTQKKNIRPGQDSSYYWIEASEVNLSTRIGSGSF 360
 QY 361 GTVYKKGWGDVAVKILKVVDPTEQFAFRNEVAVLRKTRHVNILFEGYTKDNLAV 420
 Db 361 GTVYKKGWGDVAVKILKVVDPTEQFAFRNEVAVLRKTRHVNILFEGYTKDNLAV 420
 QY 421 TQWCESSLYKHLHVQETKQFQMLDIAQTAQGMVYLAHAKNIHRDKMSNNIFLHEGL 480
 Db 421 TQWCESSLYKHLHVQETKQFQMLDIAQTAQGMVYLAHAKNIHRDKMSNNIFLHEGL 480
 QY 481 TVKIGDFGLATVKSRWSGSOQVQPTGSGVLMWMAPEVIRMQDNNPFQSDVTSYGIVLYE 540
 Db 481 TVKIGDFGLATVKSRWSGSOQVQPTGSGVLMWMAPEVIRMQDNNPFQSDVTSYGIVLYE 540
 QY 541 LMTGELPYSHINNRODIIIFMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
 Db 541 LMTGELPYSHINNRODIIIFMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
 QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTPSPRPV 648
 Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTPSPRPV 648

RESULT 3
 KMIL_CHICK STANDARD; PRT; 647 AA.
 AC P05625;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE MIL proto-oncogene serine/threonine-protein kinase (EC 2.7.1.37).
 GN C-MIL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE-Erythroblast;
 RX MEDLINE=88217299; PubMed=3285296;
 RA Koenen M., Sippel A.E., Trachmann C., Bister K.;
 RT "Primary structure of the chicken c-mil protein. Identification of
 RT domains shared with or absent from the retroviral v-mil protein.";
 RL Oncogene 2:179-185(1988).
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -|- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.

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EMBL; X07017; CAA30069.1; ;
 PIR; S00644; S00644.
 HSSP; P04049; 1FAR.
 InterPro; IPR002219; DAG_PE-bind.
 InterPro; IPR000719; Euk_pkinase.
 InterPro; IPR003116; RBD.
 InterPro; IPR004040; STY_pkinase.
 InterPro; IPR002290; Ser_thr_pkinase.
 Pfam; PF00069; pkinase; 1.
 Pfam; PF00130; DAG_PE-bind; 1.

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DR Pfam; PF02196; RBD; 1.
DR PRINTS; PR00008; DAGPE_DOMAIN.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding.
FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.
FT NP_BIND 349 609 PROTEIN KINASE.
FT BINDING 355 363 ATP (BY SIMILARITY).
FT BINDING 375 375 ATP (BY SIMILARITY).
FT ACT_SITE 468 468 BY SIMILARITY.
SQ SEQUENCE 647 AA; 73124 MW; 8E1443667312DFC0 CRC64;

Query Match 95.2%; Score 3249.5; DB 1; Length 647;
Best Local Similarity 94.6%; Pred. No. 4e-212;
Matches 613; Conservative 20; Mismatches 14; Indels 1; Gaps 1;

QY 1 MEHIQAWKTIISNGFGFKDAVFDGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIQAWKTIISNGFGKDSVDPNCISPTIVQFGYQRRASDDGKISDTKTSNTIRV 60
QY 61 FLPNKQRTVNVNRGMSLHDCMLKALKVRLGLOPECCAVFLRHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVNVNRGMSLHDCMLKALKVRLGLOPECCAVFLRHEHKGKARLDWNTDAAS 120
QY 121 LIGEELOVDFLHVPLTHNFARKFLKLAFCIDCQKLLNGFRQTCGKPFHEHCSTKV 180
DB 121 LIGEELOVDFLHVPLTHNFARKFLKLAFCIDCQKLLNGFRQTCGKPFHEHCSTKV 180
QY 181 PTMCVDMNIRQLLPNSTIGDGPALPSTMTMRBESVSRVPSQHRVSTPHATF 240
DB 181 PTMCVDMNIRQLLPNSTIGDGPALPSTMTMRBESVSRVPSQHRVSTPHATF 240
QY 241 NTSSPSSEGLSQORSTSTPNVHMVSTLPLVDSDMIEDAIRSHSESAPSSALSSPNL 300
DB 241 NTSPNPSSEGLSQORSTSTPNVHMVSTLPLVDSDMIEDAIRSHSESAPSSALSSPNM 300
QY 301 SPTGWSQKTPVPAQERAPVSGTQKKNIRPRGQDSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQERAPVSGTQKKNIRPRGQDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNILLFPGYMTKDLAIV 420
DB 361 GTVYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNILLFPGYMTKDLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQLDIAQRTAQGMVYLHAKNIITHROMKSNIFLHGL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQLDIAQRTAQGMVYLHAKNIITHROMKSNIFLHGL 480
QY 481 TVKIGDFGLATVKRSWSSQVEQPTGVSILWNAPEVIRMDNPNFSQSDVYSYGVLVE 540
DB 481 TVKIGDFGLATVKRSWSSQVEQPTGVSILWNAPEVIRMDNPNFSQSDVYSYGVLVE 540
QY 541 LMTGELPYSHINRQDIIFWVGYSAPDLSKLYKNCPRKMLRVADCVKKYKEERPLFP 600
DB 541 LMTGELPYSHINRQDIIFWVGYSAPDLSKLYKNCPRKMLRVADCVKKYKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648

RESULT 4
KRAF_XENLA STANDARD; PRT; 638 AA.
ID P09560; Q91390;
AC

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DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.1.-).
DE C-RAF.
GN Xenopus laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=99057471; PubMed=3194203;
RA le Guellec R., le Guellec K., Paris J., Philippe M.;
RT "Nucleotide sequence of Xenopus C-raf coding region.";
RN Nucleic Acids Res. 16:10357-10357(1988).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92096753; PubMed=1721855;
RA le Guellec R., Couturier A., le Guellec K., Paris J., le Fur N.,
RA Philippe M.;
RT "Xenopus c-raf proto-oncogene: cloning and expression during
RT oogenesis and early development.";
RN Biol. Cell 72:39-45(1991).
CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM
CC THE CELL MEMBRANE TO THE NUCLEUS. PART OF THE RAS-DEPENDENT
CC SIGNALING PATHWAY FROM RECEPTORS TO THE NUCLEUS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X12948; CAA31407.1; -.
CC PIR; S01930; TVXLR.
CC HSP; P04049; 1FAR.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003116; RBD.
CC InterPro; IPR004040; STY_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00130; DAG_PE-bind; 1.
CC Pfam; PF02196; RBD; 1.
CC PRINTS; PR00008; DAGPE_DOMAIN.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00109; C1; 1.
CC SMART; SM00455; RBD; 1.
CC SMART; SM00221; STYK; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding.
FT DOMAIN 138 183 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 340 600 PROTEIN KINASE.
FT NP_BIND 346 354 ATP (BY SIMILARITY).
FT BINDING 366 366 ATP (BY SIMILARITY).
FT ACT_SITE 459 459 BY SIMILARITY.
FT CONFLICT 309 309 K -> R (IN REF. 2).
SQ SEQUENCE 638 AA; 71959 MW; 1FF352BFFB528DF CRC64;

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Query Match 84.5%; Score 2885; DB 1; Length 638;
Best Local Similarity 85.3%; Pred. No. 1.6e-187;
Matches 553; Conservative 35; Mismatches 50; Indels 10; Gaps 4;

QY 1 MEHIOGAKWTLSNGFGKDAVDFGSSCSITPIVOFGYQRRASDDGLTDPKSTSWIRV 60
DB 1 MEHIOGAKWTLSNGFGKESVFGSSCSPTIVHFGYQRRASDDGLTDPKSTSWIRV 60
QY 61 FLPNKQRTVVNVNRGMSLHDCMLKALKVRGLQPECCAVFRLHHEKHKARLDWNTDAAS 120
DB 61 YLPNKQRTVVNVNRGMSLHDCMLKALKVRGLQPECCAVFRLIQDPKG-KLRLDWNTDAMS 119
QY 121 LIGELQVDFLDHVPVLTTHNPARTFLKLAFCDCIQKFLNGFCQCGYKFHCHCTKV 180
DB 120 LVGAELQVDFLDHVPVLTTHNPARTFLKLAFCDCIQKFLNGFCQCGYKFHCHCTKV 179
QY 181 PTMCVDSNIRQLLFPNSTIGDSVPALPSLTMRRMRESVRMPVSSQHRYSPTPHATF 240
DB 180 PTMCVDSNIRQLLFPNPNNIEGSHVTLPSLTMRRIGESV-RIPVSSQHRYSPTPHATF 238
QY 241 NTSPSPSEGLSQRSTSTPNVHMVSTTLFVDSRMIEDAIRSHSESASPSSPNNL 300
DB 239 STSPSPSEGLSQRSTSTPNVHMVSTTLFVDSRMIEDAIRSHSE-----SGSPNNL 291
QY 301 SPTGHSQKPTVPQAQERAPVSGTQENKIRPQRQDSSYYWEIEASEVMSLRIGSGSF 360
DB 292 SPTGHSNAKAPATHREKAASSTGQENKIRARQDSSYYWEIEASEVMSLRIGSGSF 351
QY 361 GTVYKKGWGDVAVKILKAVDPTPEQAFNEVAVLKRTHVNVILLFMGTMDKDLAIY 420
DB 352 GTVYKKGWGDVAVKILKAVDPTPEQAFNEVAVLKRTHVNVILLFMGTMDKDLAIY 411
QY 421 TQWCEGSSLYKHLHVQETKFMQFLIDIAQTQAGMDYLHAKNIHHRDKMSNIFLHEGL 480
DB 412 TQWCEGSSLYKHLHVQETKFMQFLIDIAQTQAGMDYLHAKNIHHRDKMSNIFLHEGL 471
QY 481 TVKIGDGLAVKSRWSGSOQVEQTSGLVMAPEVIRMQDNNPFQSDSYSGIVLYE 540
DB 472 TVKIGDGLAVKSRWSGSOQVEQTSGLVMAPEVIRMQDNNPFQSDSYSGIVLYE 531
QY 541 LMTGELPYSHINRDQIIFVGRGVYASPDLSKYNCPKAMKRLVADCVKVKERPLFP 600
DB 532 LMTGELPYSHINRDQIIFVGRGVYASPDLSKYNCPKAMKRLVADSVIKLRDERPLFP 591
QY 601 QILSSIELLQHSKPKINRSASEPSLHRAAHTEDINACTLTPSPKLPVF 648
DB 592 QILSSIELLQHSKPKINRSASEPSLHRAAHTEDISSCAL-TSTRLPVF 638

RESULT 5
KRAA_PIG STANDARD; PRT; 606 AA.
ID KRAA_PIG
AC O19004;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)
DE (A-Raf-1).
GN ARAF1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Landrace; TISSUE=Liver;
RX MEDLINE=97343844; PubMed=9166601;
RA Yasue H., Adams L., Ozawa A., Hanazono M., Li N., Lin Z.H.,
RA Kusumoto H.:
RT "Assignment of ARAF1 to porcine chromosome Xp11.2-pl3 by fluorescence
RT in situ hybridization".
RL Mamm. Genome 8:457-458(1997).
CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS

FROM THE CELL MEMBRANE TO THE NUCLEUS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MIL/RAF SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
BINDING DOMAIN.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: D88385; BAA232379.1; -
HSSP: P04049; 1FAR.
InterPro: IPR002219; DAG_PE-bind.
InterPro: IPR000719; Euk_pkinase.
InterPro: IPR003116; RBD.
InterPro: IPR004040; STY_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
Pfam: PF00069; pkinase; 1.
Pfam: PF00130; DAG_PE-bind; 1.
Pfam: PF02196; RBD; 1.
PRINTS: PR00008; DAGPEDOMAIN.
ProDom: PD000001; Euk_pkinase; 1.
SMART: SM00109; C1; 1.
SMART: SM00455; RBD; 1.
SMART: SM00221; STYK; 1.
PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
ATP-binding; Phorbol-ester binding.
KW DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 310 570 PROTEIN KINASE.
FT NP_BIND 316 324 ATP (BY SIMILARITY).
FT BINDING 336 336 ATP (BY SIMILARITY).
FT ACT_SITE 429 429 BY SIMILARITY.
SQ SEQUENCE 606 AA; 67538 MW; 1A7EB9A5D9DE152 CRC64;
Query Match 55.5%; Score 1893.5; DB 1; Length 606;
Best Local Similarity 60.9%; Pred. No. 1.4e-120;
Matches 375; Conservative 80; Mismatches 120; Indels 41; Gaps 9;
QY 50 DPSTSTNTRVLPNKRQTVVNRGMSLHDCMLKALKVRGLQPECCAVFRLHHEKHK 109
DB 13 EPSRAVGTVKVYLPNKRQTVVNRGMSVYDLSKALKVRGLNQDCCVYRLI---KGRK 69
QY 110 ARLDWNTDAASLIGELQVDFLDHVPVLTTHNPARTFLKLAFCDCIQKFLNGFCQTCG 169
DB 70 TVTAWDTAIPLDGEELIVLEVDVLTTHNPARTFLKLAFCDCIQKFLNGFCQTCG 129
QY 170 YKFEHCSTKVPKVCMDWS-NIRQLLFPNSTIGDSVPALPSLTMRRMRESVRMPVSS 228
DB 130 YKFEHCSSKVPKVCMDWSTNRQYVHVSQDLSGSGSRQHETPS--NRPLNEPLTPQGPSS 187
QY 229 QHRYSPTPHATFNTSSPSEGLSQRSTSTPNVHMVSTTLFVDSRMIEDAIRSHSES 288
DB 188 CTQHRDPEHPFP-----PAPANAPLQIRSTSTPNVHMVSTAPMDSLGVLTAQSFNTDA 243
QY 289 -----SPSALSS---SPNNLSPTGWSQKPTVPQAQERAPVSGTQENK 330
DB 244 AGNRGGDGAQPCSPSPASVSSGRKSPHKSPPS-----EQERKSLA---DDKKV 291
QY 331 RPRQRDSSYYWEIEASEVMSLRIGSGSGTGYKKGWGDVAVKILKVAQPTAEQAF 390
DB 292 KNLGRDSSGYWEVPPVPPSVQLLKRIQSGTGYKKGWGDVAVKILKVAQPTAEQAF 351
QY 391 RNEVAVLKRTHRVNILLFMGTMDKDLAIYQWCEGSSLYKHLHVQETKFMQFLIDIA 450
DB 391 RNEVAVLKRTHRVNILLFMGTMDKDLAIYQWCEGSSLYKHLHVQETKFMQFLIDIA 450

Db 352 KNEOVLRKTRHYVILFMGEMTRPGFAITQWCEGSSLYHLHVADTRFDMVQLIDVAR 411

Qy 451 QTAQGDYHLAKNIIHRDMKSNFIHLHGLTVKIGDFGLATVKSRWGSQQVQPTGSGVL 510

Db 412 QTAQGDYHLAKNIIHRDLKSNFIHLHGLTVKIGDFGLATVKTRWGAQPLEQPSGSGVL 471

Qy 511 WMAPEVIRMDNPFQSDVSYGIVLYELMTGELPYSHINRDQIIFMVGRYASPD 570

Db 472 WMAAEVIRMDNPFQSDVSYGIVLYELMTGELPYSHINRDQIIFMVGRYASPD 531

Qy 571 SKLYKNCPRAMKRLVADCVKKEERPLFPQILSSIELLQHSPLKINRSAPSLHRAH 630

Db 532 SKISSNCPAMRLLSDCLKFORERPLFPQILATIELLQHSPLKINRSAPSLHRTQ 590

Qy 631 TEDINACTLTSPRLP 646

Db 591 ADELPACLLSAARLVP 606

RESULT 6

KRAA_RAT

ID KRAA_RAT STANDARD; PRT; 604 AA.

AC P14056;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-).

GN ARAF1 OR A-RAF.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Fischer; Tissot-Liver;

RX MEDLINE=88217324; PubMed=3449797;

RA Ishikawa F., Takaku F., Nagao M., Sugimura T.;

RT "The complete primary structure of the rat A-raf cDNA coding region: conservation of the putative regulatory regions present in rat C-raf.";

RT C-raf.";

RL Oncogene Res. 1:243-253(1987).

CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM THE CELL MEMBRANE TO THE NUCLEUS.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MTL/RAF SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.

CC -----

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CC -----

DR EMBL; X06942; CAA30023.1; --

DR PIR; S00726; S00726.

DR HSP; P04049; 1FAR.

DR InterPro: IPR002219; DAG_PE-bind.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR003116; RBD.

DR InterPro: IPR004040; STY_pkinase.

DR InterPro: IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00130; DAG_PE-bind; 1.

DR Pfam; PF02196; RBD; 1.

DR PRINTS; PR00008; DAGPEDOMAIN.

DR ProDom; PD000001; Euk_pkinase; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00455; RBD; 1.

DR SMART; SM00221; STYK; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.

DR PROSITE; PS0081; DAG_PE_BIND_DOM_2; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;

KW ATP-binding; Phorbol-ester binding.

FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.

FT DOMAIN 308 568 PROTEIN KINASE.

FT NP_BIND 314 322 ATP (BY SIMILARITY).

FT BINDING 334 334 ATP (BY SIMILARITY).

FT ACT_SITE 427 427 BY SIMILARITY.

SQ SEQUENCE 604 AA; 67551 MW; FF24FB2170B0B115 CRC64;

Query Match 55.4%; Score 1891.5; DB 1; Length 604;

Best Local Similarity 61.7%; Pred. No. 1.9e-120;

Matches 377; Conservative 76; Mismatches 125; Indels 33; Gaps 10;

Qy 50 DPSKTSNTIRVFLPNKORTVYVNRGNSHLCHLKMALKVRGLQPECCAVFLLHEHGKK 109

Db 13 EFSRANGTVKVLPNKORTVYVNRGNSHLCHLKMALKVRGLQPECCAVFLLHEHGKK 69

Qy 110 ARLDNMTDAASLIGEEELQVDFLDHVPLTTHNFARKTEFLKAFCDICOKFLNGFRCTCG 169

Db 70 TVTAWDTAIAPLDGEELIVEVLEDPVTMNFVTKFTFLAFCDICOKFLNGFRCTCG 129

Qy 170 YKFEHSTKVTPTMCVDS-NIROLLEPNSTIGSGVPALPSLTMRMRRESVSRMPVSS 228

Db 130 YKFEHSTKVTPTMCVDS-NIROLLEPNSTIGSGVPALPSLTMRMRRESVSRMPVSS 178

Qy 229 QHRYSTHAF-----FNTSSPSESGLSQRSTSTPNVHMVSTTLPVDSRMIEDAIRS 283

Db 179 LLTQGSFPFTQQRDQEHFSPAPNPPLQRIKSTSTPNVHMVSTTLPVDSRMIEDAIRS 238

Qy 284 HSESA-----SPSALSSSPNLSPTGWSQKTPVPA-QERAPVSGTQEKNKIRPRGQ 335

Db 239 FSTDAAGRGDGPARG-SPSPASVS-SGRKSPHSLPAEQERKSLA--DEKKVKNLGY 294

Qy 336 RDSYYEIEIASFVNLSTRIGSGSGFVYKKGHGDVAVKLVVDPTPQFQAFRNEVA 395

Db 295 RDSYYEIEIASFVNLSTRIGSGSGFVYKKGHGDVAVKLVVDPTPQFQAFRNEVA 354

Qy 396 VLKTRVNIILFMGYMTKDLAIWTQWCESSLYKHLVQETKQFQIDTARQTAQG 455

Db 355 VLKTRVNIILFMGYMTKDLAIWTQWCESSLYKHLVQETKQFQIDTARQTAQG 414

Qy 456 MDYLHAKNIIHRDMKSNFIHLHGLTVKIGDFGLATVKSRWGSQQVQPTGSGVLMAPE 515

Db 415 MDYLHAKNIIHRDMKSNFIHLHGLTVKIGDFGLATVKSRWGSQQVQPTGSGVLMAPE 474

Qy 516 VIRMDNPFQSDVSYGIVLYELMTGELPYSHINRDQIIFMVGRYASPDLSKLYK 575

Db 475 VIRMDNPFQSDVSYGIVLYELMTGELPYSHINRDQIIFMVGRYASPDLSKLYK 534

Qy 576 NCPAMRRLVADCVKKEERPLFPQILSSIELLQHSPLKINRSAPSLHRAHRTEDIN 635

Db 535 NCPAMRRLVADCVKKEERPLFPQILSSIELLQHSPLKINRSAPSLHRAHRTEDIN 593

Qy 636 ACTLTSPRLP 646

Db 594 ACTLTSPRLP 604

RESULT 7

KRAA_MOUSE

ID KRAA_MOUSE STANDARD; PRT; 604 AA.

AC P04627; Q99J44; Q9CTT5; Q9D6R6; Q9DBU7;

DT 13-AUG-1987 (Rel. 05, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-).

GN ARAF1 OR ARAF OR A-RAF.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.1-)
 DE (A-Raf-1) (Proto-oncogene Pks).
 GN ARAF1 OR Pks OR PKs2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=87146380; PubMed=3029685;
 RA Beck T.W., Huleihel M., Gunnell M., Bonner T.L., Rapp U.R.;
 RT "The complete coding sequence of the human A-Raf-1 oncogene and
 RL transforming activity of a human A-Raf carrying retrovirus.";
 RL Nucleic Acids Res. 15:595-609(1987).
 RP SEQUENCE FROM N.A.
 RP MEDLINE=94292185; PubMed=8020955;
 RC TISSUE=Placenta;
 RX MEDLINE=94292185; PubMed=8020955;
 RA Lee J.-E., Beck T.W., Brennscheidt U., DeGennaro L.J., Rapp U.R.;
 RT "The complete sequence and promoter activity of the human A-Raf-1
 RL gene (ARAF1).";
 RL Genomics 20:43-55(1994).
 RP SEQUENCE OF 292-589 FROM N.A.
 RX MEDLINE=86313571; PubMed=3529082;
 RA "Pks, a raf-related sequence in humans.";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:6312-6316(1986).
 CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN UROGENITAL TISSUES (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
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 CC
 DR EMBL; X04790; CAA28476.1; -;
 DR EMBL; L24038; AAA65219.1; -;
 DR EMBL; U01337; AAB03517.1; -;
 DR EMBL; M13829; AAB08754.1; -;
 DR PIR; A26439; TVHDAF.
 DR PIR; A23541; TVHUPK.
 DR HSP; P04049; IFAR.
 DR Genew; HGNC:646; ARAF1.
 DR MIM; 311010; -;
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003116; RBD.
 DR InterPro; IPR004040; STY_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00130; DAG_PE-bind; 1.
 DR Pfam; PF02196; RBD; 1.
 DR PRINTS; PR000008; DAGPEDOMAIN.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00455; RBD; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM.1; 1.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM.2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
 KW ATP-binding; Phorbol-ester binding.
 FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 310 570 PROTEIN KINASE.
 FT NP_BIND 316 324 ATP (BY SIMILARITY).
 FT BINDING 336 336 ATP (BY SIMILARITY).
 FT ACT_SITE 429 429 BY SIMILARITY.
 FT CONFLICT 368 378 L -> P (IN REF. 3).
 FT CONFLICT 378 378 F -> V (IN REF. 3).
 FT CONFLICT 469 469 S -> P (IN REF. 3).
 FT CONFLICT 478 478 I -> T (IN REF. 3).
 SQ SEQUENCE 606 AA; 67585 MW; D23E5711304AA68 CRC64;
 Query Match 55.4%; Score 1889.5; DB 1; Length 606;
 Best Local Similarity 61.9%; Pred. No. 2.6e-120;
 Matches 376; Conservative 76; Mismatches 132; Indels 23; Gaps 9;
 QY 50 DPSKTSNTIRVFLPNKQRTVVNRGMSLDCLMKALKVGRLOPECCAVFLLHEHCKK 109
 DB 13 EFSRAVGTIVKTVLPNKRQRTVVTRDMSVYDLDKALKVGRGLNQDCCVYIRLI---GRRK 69
 QY 110 ARLDWNTDAASLIGEELOVDLDRHVLTHNFARKTLKAFCDICQKFLNGFCQTCG 169
 DB 70 TVTAWDTAIAPLDGEELIVEVLEVDVPLTMHNFVKTFFSLAFCDLFLHGFRCQTCG 129
 QY 170 YKFEHCSTKVTMCVDNSNIRQLLLFPNSTI-GDSGVDPALPSLTMRMRRESVSRMPVSS 228
 DB 130 YKFEHCSTKVTMCVDNSNIRQLLLFPNSTI-GDSGVDPALPSLTMRMRRESVSRMPVSS 187
 QY 229 OHRYSTPHAFNTSSPSSEGLSORSTSTPNVHMVSTTLTPVDSMTIE-----DA 280
 DB 188 RQHCDEHPFP-----PAPANAPLQIRSTSTPNVHMVSTTAPMDSNLIQLTGQSFSDA 243
 QY 281 IRSHSESASPSSALSSPNNLSPGTGWSQPKTPVPA-QRERAPVSGTQEKNIKPRQDSS 339
 DB 244 AGSRGSDGTGRGSPSPASVS-SGRKSPHSKSPAQRERKSLA--DDKKVKNLGYRDSG 300
 QY 340 YWYEASEVMSLSTRIGSGFVYKGVHGDVAVKILKVDPDTPQEQAFRNEVAVLRK 399
 DB 301 YWYEVPPSEVQLLRIGTSGFVYKGVHGDVAVKILKVDPDTPQEQAFRNEVAVLRK 360
 QY 400 TRHVNILLFMGYMTKDLAIVTQWCEGSLYKHLHVQETKFFOMFOLIDARTAGMDYL 459
 DB 361 TRHVNILLFMGYMTKDLAIVTQWCEGSLYKHLHVQETKFFOMFOLIDARTAGMDYL 420
 QY 460 HAKNIITHRDMKNNIFLHEGLVFKIGDGLATVTKSRWSGSGQVQPTQSVLMAPEVIRM 519
 DB 421 HAKNIITHRDLKSNIFLHEGLVFKIGDGLATVTKSRWSGSGQVQPTQSVLMAPEVIRM 480
 QY 520 QDNPFOSDYVSYGVILYELMTGELPYSHNNRDOIIIFWVGRCYASPDLSKLYKNCPK 579
 DB 481 QDPNPFOSDYVSYGVILYELMTGELPYSHNNRDOIIIFWVGRCYASPDLSKLYKNCPK 540
 QY 580 AMKRLVADCVKRVKKEERPLFPQILSSIELLQSLPKINRSASEPSLHRAATEDINACTL 639
 DB 541 AMRRLSDCLKFQREERPLFPQILATIELQSLPKIERSASEPSLHR-TQADELPACIL 599
 QY 640 TTSPLRP 646
 DB 600 SAARLYP 606
 RESULT 9
 KML_AVIMH STANDARD; PRT; 380 AA.
 ID KML_AVIMH
 AC P00531;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase transforming protein ml
 DE (EC 2.7.1.37).
 GN V-MIL OR V-MHT.

OS Avian retrovirus MH2.
 OC Viruses; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxID=11870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191511; PubMed=6325930;
 RA Sutcliffe P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,
 RA "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of
 RT murine retroviral oncogene v-raf";
 RL Nature 309:85-88(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84121298; PubMed=6320371;
 RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
 RT "A common oncogene sequence transduced by avian carcinoma virus MH2
 RL and by murine sarcoma virus 3611";
 RN Science 223:813-816(1984).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- DISEASE: BY ITSELF THE V-MIL ONCOGENE HAS ONLY WEAK TRANSFORMING
 CC CAPACITY BUT IT ABOLISHES THE GROWTH FACTOR REQUIREMENTS OF AVIAN
 CC MACROPHAGES TRANSFORMED BY OTHER ONCOGENES.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-MT OR GAG-MIL
 CC POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X00534; CAA25211.1; ALT_INIT.
 DR PTR; A00639; TVFVNM.
 DR HSP; P08631; IAD5.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR004040; STY_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PolyProtein; Serine/threonine-protein kinase; Transferase; Oncogene;
 KW ATP-binding.
 FT DOMAIN 82 341 PROTEIN KINASE.
 FT NP_BIND 88 96 ATP (BY SIMILARITY).
 FT BINDING 108 108 ATP (BY SIMILARITY).
 FT ACT_SITE 201 201 BY SIMILARITY.
 FT CONFLICT 211 211 G -> E (IN REF. 2).
 SQ SEQUENCE 380 AA; 42853 MW; 6498695FB7EBE5D CRC64;
 Query Match 55.3%; Score 1888.5; DB 1; Length 380;
 Best Local Similarity 94.7%; Pred. No. 1.7e-120;
 Matches 360; Conservative 12; Mismatches 7; Indels 1; Gaps 1;
 QY 269 TLPVDSRMTEIDAIRHSEASPSALSSPNNSPTGWSQPKTPVPAQERAPVSGTQKN 328
 DB 2 THPVDSEIIDAIRHSEASPSASGSPNNMSPGWSQPKTPVPAQERAPVSGTQKN 61
 QY 329 KIRPRQDSYYWEIEASEVLMSTRIGSGFTYVKGWHDGVAVKILKVVDPPEQFQ 388
 DB 62 KIRPRQDSYYWEIEASEVLLSTRIGSGFTYVKGWHDGVAVKILKVVDPPEQFQ 121
 QY 389 AFRNEVAVLRKTHVNNILLFMGYMKDNLAIYVQNCESGLYKHLHVQETKFMQLIDI 448
 DB 122 AFRNEVAVLRKTHVNNILLFMGYMKDNLAIYVQNCESGLYKHLHVQETKFMQLIDI 181
 QY 449 ARQTAQGM DY LKAKNI IHRDMKSNIFLHGGLTVKIGDFGLATVKSRWSSGQVEQPTGS 508

Db 182 ARQTAQGM DY LKAKNI IHRDMKSNIFLHGGLTVKIGDFGLATVKSRWSSGQVEQPTGS 241
 QY 509 VLMAPEVIRMDNNPFSQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGKGYASP 568
 Db 242 ILMAPEVIRMDNSNPFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGKGYASP 301
 QY 569 DLSKLYKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPSSLHRA 628
 Db 302 DLSKLYKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPSSLHRA 361
 QY 629 AHTEIDINACTLTITSPRLPVF 648
 Db 362 SHTEIDINACTLTITSPRLPVF 380
 RESULT 10
 KRAB_HUMAN
 ID KRAB_HUMAN STANDARD; PRT; 765 AA.
 AC P15056;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE B-raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)
 DE (p94) (v-Raf murine sarcoma viral oncogene homolog B1).
 GN BRAF OR BRAF1 OR RAFB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-Testis;
 RX MEDLINE=923735040; PubMed=1508179;
 RA Stephens R.M., Sthanandam G., Copeland T.D., Kaplan D.R., Rapp U.R.,
 RA Morrison D.K.;
 RT "95-kilodalton B-Raf serine/threonine kinase: identification of the
 RL protein and its major autophosphorylation site";
 RL Mol. Cell. Biol. 12:3733-3742(1992).
 RN [2]
 RP SEQUENCE OF 116-765 FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=91133728; PubMed=2284096;
 RA Sthanandam G., Kolch W., Duh F.-M., Rapp U.R.;
 RT "Complete coding sequence of a human B-raf cDNA and detection of
 RT B-raf protein kinase with isozyme specific antibodies";
 RL Oncogene 5:1775-1780(1990).
 RN [3]
 RP SEQUENCE OF 438-765 FROM N.A.
 RX MEDLINE=88302178; PubMed=3043188;
 RA Ikawa S., Fukui M., Ueyama Y., Tamaoki N., Yamamoto T., Toyoshima K.;
 RT "B-raf, a new member of the raf family, is activated by DNA
 RT rearrangement";
 RL Mol. Cell. Biol. 8:2651-2654(1988).
 CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF
 CC HIPPOCAMPAL NEURON.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: CEREBRUM AND TESTES.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -----
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[illegible]

Pfam: PF02196; RBD; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00221; STYKc; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Proto-oncogene; Transferase; Serine/threonine-protein kinase;
KW ATP-binding; Nuclear protein; Alternative splicing; Zinc;
Phorbol-ester binding; Phosphorylation.
FT DOMAIN 122 129
FT FT DOMAIN 122 129 POLY-SER.
FT FT DOMAIN 235 280 PHORBOL-ESTER AND DAG BINDING.
FT FT DOMAIN 248 280 CYS-RICH.
FT FT DOMAIN 497 757 PROTEIN KINASE.
FT FT NP_BIND 503 511 ATP (BY SIMILARITY).
FT FT BINDING 523 533 ATP (BY SIMILARITY).
FT FT ACT_SITE 616 616 BY SIMILARITY.
FT FT VARSPIC 393 432 MISSING (IN SHORT ISOFORM).
FT SEQUENCE 806 AA; 89365 MW; 8E3FA4D5274FB75C CRC64;

Query Match 53.1%; Score 1814; DB 1; Length 806;
Best Local Similarity 52.8%; Pred. No. 4.9e+115;
Matches 382; Conservative 80; Mismatches 149; Indels 112; Gaps 15;

QY	9	KTISNGFGFK-----DAVFDGGSSCIPTTVQFQGYRRASDDGKLTDPSKTSNTIRVF	61
DB	101	ESMGKGTDFSVSSASTDTVAASSSSLSVAPSLVSIVQNPTMSRNPSPKPIVRVF	160
QY	62	LPNKORTVVNVRNGMSLHCLMKALKYRGLOPECCAVFRLLHEHKRKARDWNTDAASL	121
DB	161	LPNKORTVVPARCGVTVDRLSKALLMRGLIPECCAVRI--QDGKKPGWDTDISWL	217
QY	122	IGEEQLVDFLDHVLTTHNFARKFLKAFCDICOKELLNGFRQCOTCYGFHFHCSTKVP	181
DB	218	TGEELHVEYLENVPLTTHNFVRKTFFTLAFDCFKLLFOGRCQTCTCYGFHFRCSTEV	277
QY	182	TMCVDWSNIROLLL-----FPNSTIGDS-GVPALPSLTMR	215
DB	278	LMCVNYDQLDLFLVSKFFEHPHSIQEETTLGETTPAGSGTSPVPPSDSVGPPILPS	333
QY	216	RMRESVRMPVSSQHRYSTPHAFNTNTSSPSSEGLSQQRSTSTPNVHMVSTPLPYDSR	275
DB	334	-----PSPSK---SIPIQPFRPADEHRNQFGORDRSSAPNVH-INIEPVN--	378
QY	276	MIEDAIRSHS-----ESAPSAL-----	293
DB	379	-IDDLIRQGVGREGAPLNQLMRLCKRYQSTRPSPLLHVSPIETVDFEPGPVFRGSTAG	437
QY	294	-----SSPNLSPGTSQPKTPVPAQREAPRVSGTGQENKIRPRGORDSSYYWELEAS	347
DB	438	LSATPPASLPGSLTNVKALQ-KSGCP-QREKRSSSEDNRNMKTGLRRDSDDWELPDG	495
QY	348	EVMALSTRIGSGSGFYVKGKHGDVAVKILKVDPDTPTEQFAEFNEVAVLKTRHYNNILL	407
DB	496	QITVGORIGSGSGFYVKGKHGDVAVKMLNVTAAPTQQQAQFNKEVGLKTRHYNNILL	555
QY	408	FNGYWTKNLAIVTCWGCSGLYKHLHVQETKFQWFQFLDIARTAGDMYLHAKNIIHR	467
DB	556	FMYGTKPOLAIVTCWGCSGLYHLHIETFKFMIKLIDIARTAGDMYLHAKSIHR	615
QY	468	DKMSNIFUHEGLTVKIGDFGLATVKVRSWGSQQVEQPTGSLVMAPEVIRMQDNPFSE	527
DB	616	DLKSNFIUFHEDLTWKIGDFGLATVKVRSWGSQGHQFEQLSGSILMAPEVIRMQDNPFSE	675
QY	528	QSDVSYGIVLYELMTGELYSHINNRRDQIIFMVGRGYASPDLASKLYKNCPKAKMLRAD	587
DB	676	QSDVYAFGIVLYELMTGQLPSYNINRRDQIIFMVGRGLYSPDLASKLVNSCNCPKAKMLMAE	735
QY	588	CYVKKVEERPLPQILSIELLQHSPLKPINKASSEPSSLRAA-HTEDIN--ACTLTTSR	644

KW ATP-binding; Nuclear protein; Alternative splicing; Zinc;
FT Phorbol-ester binding; Phosphorylation.
FT DOMAIN 122 129 POLY-SER.
FT DOMAIN 235 280 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 248 280 CYS-RICH.
FT DOMAIN 497 757 PROTEIN KINASE.
FT NP_BIND 503 511 ATP (BY SIMILARITY).
FT BINDING 523 523 ATP (BY SIMILARITY).
FT ACT_SITE 616 616 BY SIMILARITY.
FT VARSPIC 393 432 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 807 AA; 89521 MW; 199700AE65242FB7 CRC64;

Query Match 53.1%; Score 1814; DB 1; Length 807;
Best Local Similarity 52.8%; Pred. No. 4.9e-115;
Matches 382; Conservative 80; Mismatches 149; Indels 112; Gaps 15;

QY 9 KTIISNGFGFK-----DAVFDGSSCISPTIVQFGYORRASDDGKLTDPSTNTIRVF 61
Db 101 ESMGNGTDFSVSSASTDTVASSSSSSLSVAPSSLSVYQNPDTMSRNNPKSPQKPIVRVF 160
QY 62 LPNKQRTVYVRNGMSLHDCMLKALKVRLQPECAVFLHEHKKARLDWNTDAASL 121
Db 161 LPNKQRTVYVRCGVTVRDSLKKALMRGLIPECCAVYRI--QDGEKKPIGWDTDISWL 217
QY 122 ICEELQVDFLDHVPVLTTHNFARKTFLKAPDCICQKFLNGFRQTCGYKHEHCSTKVP 181
Db 218 TGEELHVEVLENVPLTTHNFVRKTFPTLAFDCFCKLLFQGRQTCGYKHEHCSTKVP 277
QY 182 TMCVDWSNIQRLLL-----FPNSTIGDS-GVPALPSLTMR 215
Db 278 LMCVYDQLDLFLVSKFFHEHPISQETTLGETTPASGSYFVSPDSVGVGPILPS---- 333
QY 216 RMRESVRMPYSSQHYRTPHAFNTSPSEGSLSQRQSTPNVYVSTLPVDSR 275
Db 334 -----PSPSK---SIPIQPPRPADHRNQFGORDRSSAPNVH-INTIEPVN-- 378
QY 276 MLEDAIRSHS-----ESAPSPAL----- 293
Db 379 -IDDLIRQGVREGAPLNQLMRCURKYQSRTPSLLHSVPSEIVDFEPGPVFRGSTAG 437
QY 294 -----SSPNLSPSGSQKTPVPAQRERAPVSGTQEKKNIRPRGQDSSSYWEIEAS 347
Db 438 LSATPPASLPGLSTNVKALQ-KSPGP-QREKSSSSSEDRNMKTLCRRDSSDDWEIPDG 495
QY 348 EVMFLSTRIGSGFGVYKKGHDGVAVKILKVDPDTPQFOAFNEVAVLRKTRHVNILL 407
Db 496 QITVGQRIGSGFGVYKKGHDGVAVKILKVDPDTPQFOAFNEVAVLRKTRHVNILL 555
QY 408 FMGYWTKDNLAIYVQWCEGSSLYKHLVQETKFMQFOLIDTARQTAQGMVYLHAKNIHR 467
Db 556 FMGYSTKQLQALVYVQWCEGSSLYKHLVQETKFMQFOLIDTARQTAQGMVYLHAKNIHR 615
QY 468 DMKSNIFLHEGLTVKIGDFGLATVYKSRWSSQVQPTGSLVMAPEVIRMDNNPFSE 527
Db 616 DLKSNIFLHEGLTVKIGDFGLATVYKSRWSSQVQPTGSLVMAPEVIRMDNNPFSE 675
QY 528 QSDVYSYGLVYELMTGELPYSINNRDQIIFWVGRGYASPDLSKLYKNCPKMKRLVAD 587
Db 676 QSDVYAFGLVYELMTGELPYSINNRDQIIFWVGRGYASPDLSKLYKNCPKMKRLVAD 735
QY 588 CVYKVKERPLFPQILSSTELIQLHSLPKINRSASEPSLHRAA-HTEDIN--ACTLTSPR 644
Db 736 CLKKRDRLFPQILSSTELIQLHSLPKINRSASEPSLHRAA-HTEDIN--ACTLTSPR 692
QY 645 LPV 647
Db 793 TPI 795

RESULT 13
KRAF_MSV36
ID KRAF_MSV36 STANDARD; PRY; 323 AA.
AC P00532;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase transforming protein raf (EC 2.7.1.1-).
GN V-RAF.
OS Murine sarcoma virus 3611.
OC Viruses; Retroviridae; Retroviridae; Mammalian type C retroviruses.
OX NCBI_TaxID=11812;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84121298; PubMed=6320371;
RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
RT "A common onc gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";
RL Science 223:813-816(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84172180; PubMed=6324342;
RA Mark G.E., Rapp U.R.;
RT "Primary structure of v-raf: relatedness to the src family of
oncogenes.";
RL Science 224:285-289(1984).
CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-RAF
POLYPEPTIDE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: K01691; AAA46579.1; ALT_INIT.
DR PIR: A00538; TVMVF8.
DR HSP: P12931; IFMK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW Polyprotein; Serine/threonine-protein kinase; Transferase; Oncogene;
ATP-binding.
FT DOMAIN 24 284 PROTEIN KINASE.
FT NP_BIND 30 38 ATP (BY SIMILARITY).
FT BINDING 50 50 ATP (BY SIMILARITY).
FT ACT_SITE 143 143 BY SIMILARITY.
SQ SEQUENCE 323 AA; 36883 MW; 52A5423A66E362F3 CRC64;

Query Match 48.5%; Score 1654; DB 1; Length 323;
Best Local Similarity 97.2%; Pred. No. 9.3e-105;
Matches 314; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 326 EKNKIRPRGQDSSYWEIEASEVMSLSTRIGSGFGTVYKKGHDGVAVKILKVDPDTPPE 385
Db 1 EKNKIRPRGQDSSYWEIEASEVMSLSTRIGSGFGTVYKKGHDGVAVKILKVDPDTPPE 60
QY 386 QFOAFNEVAVLRKTRHVNILLFMQFOLIDTARQTAQGMVYLHAKNIHR 445
Db 61 QFOAFNEVAVLRKTRHVNILLFMQFOLIDTARQTAQGMVYLHAKNIHR 120
QY 446 IDTARQTAQGMVYLHAKNIHRDMKNNIFLHGLTVKIGDFGLATVYKSRWSSQVQVPEP 505
Db 121 IDTARQTAQGMVYLHAKNIHRDMKNNIFLHGLTVKIGDFGLATVYKSRWSSQVQVPEP 180
QY 506 TGSVLMMAPEVIRMDNNPFSEFQSDVYSYGLVYELMTGELPYSINNRDQIIFWVGRGY 565
Db 506 TGSVLMMAPEVIRMDNNPFSEFQSDVYSYGLVYELMTGELPYSINNRDQIIFWVGRGY 565

Db 181 TGSVLWMAPEVIRMQDDNPFQSDVYSYGVIVLYELMAGELPYAHINNRDQIIFWVGROY 240
Qy 566 ASDLSKLYKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLQHSLEPKINRSASEPSL 625
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 ASDLSRLYKNCPRKAIKRLVADCVKVKKEERPLFPQILSSIELLQHSLEPKINRSASEPSL 300
Qy 626 HRAAHTEDINACTLTTSPLPVF 648
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 HRAAHTEDINACTLTTSPLPVF 323

RESULT 14

KRAF_DROME STANDARD; PRT; 781 AA.
AC P11346;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAF homolog serine/threonine-protein kinase drap-1 (EC 2.7.1.1-)
DE (Pole-hole protein).
GN PHL OR DRAF-1 OR D-RAF.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88283647; PubMed=3135183;
RA Nishida Y., Hata M., Ayaki T., Ryo H., Yamagata M., Shimizu K.,
RA Nishizuka Y.;
RT "Proliferation of both somatic and germ cells is affected in the
RT Drosophila mutants of raf proto-oncogene.";
RL EMBO J. 7:775-781(1988).
RN [2]
RP SEQUENCE OF 465-753 FROM N.A.
RX MEDLINE=87257926; PubMed=3037346;
RA Mark G.E., Macintyre R.J., Digan M.E., Ambrosio L., Perrimon N.;
RA "Drosophila melanogaster homologs of the raf oncogene.";
RL Mol. Cell. Biol. 7:2134-2140(1987).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=93140754; PubMed=8423783;
RA Sprenger F., Torsocclair M.M., Morrison D.K.;
RA "Biochemical analysis of torso and D-raf during Drosophila
RT embryogenesis: Implications for terminal signal transduction.";
RL Mol. Cell. Biol. 13:1163-1172(1993).
CC -1- FUNCTION: SERINE/THREONINE KINASE REQUIRED IN THE EARLY EMBRYO
CC FOR THE FORMATION OF TERMINAL STRUCTURE. ALSO REQUIRED DURING
CC THE PROLIFERATION OF IMAGINAL CELLS. MAY ACT DOWNSTREAM OF RAS1
CC IN THE SEV SIGNAL TRANSDUCTION PATHWAY.
CC -1- P-TM: EXTENSIVELY PHOSPHORYLATED AT 1 TO 2 H AFTER EGG LAYING.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.

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or send an email to license@isb-sib.ch).

DR EMBL: X07181; CAA30166.1; ALT_INIT.
DR EMBL: M16598; -: NOT_ANNOTATED_CDS.
DR PIR: S00393; TVFDF.
DR HSP: P04049; IRFA.
DR FlyBase: FBgn0003079; phl.
DR InterPro: IPR002219; DAG_pe-bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003116; RBD.

DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00130; DAG_pe-bind; 1.
DR Pfam: PF02196; RBD; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; Cl; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS0081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
KW Phorbol-ester binding; Phosphorylation.
FT DOMAIN 265 310 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 471 732 PROTEIN KINASE
FT NP_BIND 477 485 ATP (BY SIMILARITY).
FT BINDING 497 497 ATP (BY SIMILARITY).
FT ACT_SITE 590 590 P -> A (IN REF. 2).
FT CONFLICT 495 495 KKT -> RKA (IN REF. 2).
FT CONFLICT 520 522 G -> R (IN REF. 2).
FT CONFLICT 571 571 RRHS -> PQAL (IN REF. 2).
FT CONFLICT 700 703
SQ SEQUENCE 781 AA; 88794 MW; DEAD54762249EADC CRC64;

Query Match 39.8%; Score 1360; DB 1; Length 781;
Best Local Similarity 46.3%; Pred. No. 2.2e-84;
Matches 303; Conservative 86; Mismatches 194; Indels 72; Gaps 16;

QY 32 IVQFGYQRRASDDGKLD-----PSKTSNT-----IRVFLPNKORTVVVNRGMSL 78
Db 146 ILQOORQLARVHGTDLTSLGSPGSCGTLTROPKILLRAHLPNOORTSVEVIGVRL 205
QY 79 HDLKMALKVGLQPECCAVFLLHEHGKKAARLDWNTDAALGEEQLQVDFLDHVLPTT 138
Db 206 CDALMKALKRLQTLTDMCEVST---THSGRHI-IPWHDIGTLHVEEIVRLDFFPIRT 261
QY 139 ---HNFARKTFLKLAFCDCIKQKFLNGFCQCYKFEHCSTKYPTMCVDW--SNIRQL 193
Db 262 HIKHQIIRKTFEFLVFCGCRLLFTGYSCQCFRHFQRCANRVMLCQPPMDSYQL 321
QY 194 LLEPNSTICDSGVPALPSLTMRMRSEVSRPVSVQSHRYSTPHATFTSS--PSEGS- 250
Db 322 LLAEND---DNGV-GFPG-----RGTAVRFNMSSRSRRSSSSSSSSSSSSSGN 371
QY 251 -----LSQRSTSTPNV---HMVSTTLPVDSRMIEDA-----IRSHSESASPSA 292
Db 372 HRQGRPRISQDDRSNSAPNVCINNIRSVTSEVQSLINQARPPPLPHCTDHSNSTQASP 431
QY 293 LSSPPNLSPTGWSQKTPVPAQRAPVSGTQEKNIKIRPGORDSSYYWEIEASEVMLS 352
Db 432 TSTLKH-----RPRASADESNKLL-ROAKSSEENWNLAEILIG 474
QY 353 TRIGSSFGTVYKKGWHDVAVKILKVDPTEQQAQAFNEVAVLKRTHVILLFMGVN 412
Db 475 PRIGSGFGTVYRAHVGPPVVKTLNVKTPSPAQLQAFKNEVAMLKTRHCVILLFMGCV 534
QY 413 TKDNLAIVTQWCEGSSLYKHLHVQETKQFOMFOLIDIARTAOQMDYLAHAKNIHRDKSN 472
Db 535 SKPSLAIVTQWCEGSSLYKHHVSETKFKLNTLIDIGROVAGMDYLAHAKNIHRDLKSN 594
QY 473 NIFLHGLAVKIGDFGLATVKRWGSSQVQEPQTSVLWMAPEVIRMQDNNPFQSDVY 532
Db 595 NIFLHEDLSVKIGDFGLATAKTAWSGEKANQPTGSLWMAPEVIRMQELNPFQSDVY 654
QY 533 SYGIVLYELMTGELPYSHINNRDQIIFWVGROYASPDLSKLYKNCPRAMKRLVADCVKV 592
Db 655 AFGIVMYELLAECPLPYGHISNKKDQILFMVGRGLLDDMSQVRSDDARRHRSKRLAEIC 714
QY 593 KEERPLFPQILSSIELLQHSLEPKINRSASEPSLHRAAHTEDINACTLTTSPLPV 647

Search completed: July 9, 2003, 09:45:27
Job time : 29 secs

Query Match	39.1%	Score 1336;	DB 1;	Length 450;
Best Local Similarity	69.1%;	Pred. No. 4.4e-83;		
Matches	264;	Conservative 45;	Mismatches 59;	Indels 14; Gaps 6;
276 MIEDATRS--- <td>: : </td> <td> : : :</td> <td>:</td> <td> : : : :</td>	: :	: : :	:	: : : :
4 VIKDLIRDQGVREGSGTAGLSATPASLPGSLTNVKALQKSPG-QRERSKSSSESDRN 62	:	:	:	:
329 KIPRCGRDSYYWETEASEVMLSRTIGSGSGFTYVKGWHGDVAVKILKYVDTPPQQF 388	::: :	: : : :	:	: : : :
63 RMTKLRRDSSDDWEIPDQGITVGRISSGSFGTYVKGWHGDVAVKMLNTAFTPQQLQ 122	:	:	:	:
389 AFNEAVAILRKTRHHYNILLFWGYMFKDNLAIVTWCEGSSLYKKLHVQETKFQMFLIDI 448	: :	: :	: :	: :